

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX WPI: 2000-365619/31.
DR N-PSDB: MADD00519.
XX
XX Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
XX Claim 44; Page 172; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MTDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT1 from human brain.
XX
XX Sequence 297 AA:
S0
Query Match 100.0%; Score 1553; DB 21; Length 297;
Best Local Similarity 100.0%; Pred. No. 3, 2e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGDHMSFLKDFLAGAVAAVSKTAVADIERVKLLQVQHASKOISAEKQKGIIDCYVR 60
DB 1 MGDHMSFLKDFLAGAVAAVSKTAVADIERVKLLQVQHASKOISAEKQKGIIDCYVR 60
QY 61 IPKEGFLSPWRGNLANVIRYFPTQALNFAFKDKYKQFLGVDVRHKOFWRYFAGNLASG 120
DB 61 IPKEGFLSPWRGNLANVIRYFPTQALNFAFKDKYKQFLGVDVRHKOFWRYFAGNLASG 120
QY 121 GAAGATSLCFYPPDLFATRLAADYGRRAOREFHGLGCIIRKSDLRGLYOGFNVSV 180
DB 121 GAAGATSLCFYPPDLFATRLAADYGRRAOREFHGLGCIIRKSDLRGLYOGFNVSV 180
QY 181 OGIIITRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLLSPFTVRRMMQ 240
DB 181 OGIIITRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLLSPFTVRRMMQ 240
QY 241 SGRKGADIMYGTVDCKWRIKADGAKAFKFGANSNVLRGNGAFVLYLDEIKRYV 297
DB 241 SGRKGADIMYGTVDCKWRIKADGAKAFKFGANSNVLRGNGAFVLYLDEIKRYV 297
RESULT 2
AAU01198
ID AAU01198 standard; Protein: 297 AA.
XX
XX AAU01198;
XX
XX 07-SEP-2001 (first entry)
XX
XX Human adenine nucleotide translocator-1 (ANT-1) protein.
XX
XX Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX

OS Homo sapiens.
XX
XX WO200132876-A2.
XX
XX 10-MAY-2001.
XX
XX 03-NOV-2000; 2000WO-US30535.
XX
XX 03-NOV-1999; 99US-0434354.
XX
XX (MITO-) MITOKOR.
XX
XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
PI Velicelc G, Davis RE;
XX WPI: 2001-291054/30.
DR N-PSDB: MADS05901.
XX
XX New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
XX Disclosure; Fig 2; 186pp; English.

The present sequence represents human adenine nucleotide translocator-1 (ANT-1) protein. ANT proteins are mitochondrial permeability transition (MPT) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.

XX
XX Sequence 297 AA:
S0
Query Match 100.0%; Score 1553; DB 22; Length 297;
Best Local Similarity 100.0%; Pred. No. 3, 2e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGDHMSFLKDFLAGAVAAVSKTAVADIERVKLLQVQHASKOISAEKQKGIIDCYVR 60
DB 1 MGDHMSFLKDFLAGAVAAVSKTAVADIERVKLLQVQHASKOISAEKQKGIIDCYVR 60
QY 61 IPKEGFLSPWRGNLANVIRYFPTQALNFAFKDKYKQFLGVDVRHKOFWRYFAGNLASG 120
DB 61 IPKEGFLSPWRGNLANVIRYFPTQALNFAFKDKYKQFLGVDVRHKOFWRYFAGNLASG 120
QY 121 GAAGATSLCFYPPDLFATRLAADYGRRAOREFHGLGCIIRKSDLRGLYOGFNVSV 180
DB 121 GAAGATSLCFYPPDLFATRLAADYGRRAOREFHGLGCIIRKSDLRGLYOGFNVSV 180
QY 181 OGIIITRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLLSPFTVRRMMQ 240
DB 181 OGIIITRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLLSPFTVRRMMQ 240
QY 241 SGRKGADIMYGTVDCKWRIKADGAKAFKFGANSNVLRGNGAFVLYLDEIKRYV 297
DB 241 SGRKGADIMYGTVDCKWRIKADGAKAFKFGANSNVLRGNGAFVLYLDEIKRYV 297
RESULT 3

AAU10378
 ID AAU10378 standard; protein; 297 AA.
 XX
 AC AAU10378;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human adenine nucleotide translocator 1 (ANT1).
 XX
 KW Human; adenine nucleotide translocator; ANT;
 KW mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 XX
 PN MO200185944-A2.
 PD 15-NOV-2001.
 PF 11-MAY-2001; 2001MO-US15416.
 PR 11-MAY-2000; 2000US-0569327.
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Milley SE, Miller SM, Szabo TR;
 PI Ghosh SS, Moos WR, Pel Y, Carroll AK;
 DR WPI: 2002-055598/07.
 DR N-PSDB: AAS16688.
 XX
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide
 XX
 XX Claim 44; Fig 2; 147pp; English.
 CC The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT1.
 XX
 SQ Sequence 297 AA:
 Query Match 100.0%; Score 1553; DB 23; Length 297;
 Best Local Similarity 100.0%; Pred. No. 3.2e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MGHANSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASQISAEEKYKGIIDCVR 60
 DB 1 MGHANSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASQISAEEKYKGIIDCVR 60
 OY 61 IPREGFLSFMGNLANVIRYPTQALNFAFKDKYKOLFLGVDNRHKKFRRYFAGNLASG 120
 DB 61 IPREGFLSFMGNLANVIRYPTQALNFAFKDKYKOLFLGVDNRHKKFRRYFAGNLASG 120
 OY 121 GAAGATSLCVYPLDFARTLADVGRRAOREFHGLGDCIITKIFKSGDLGLYGFNVSV 180
 DB 121 GAAGATSLCVYPLDFARTLADVGRRAOREFHGLGDCIITKIFKSGDLGLYGFNVSV 180
 OY 121 GAAGATSLCVYPLDFARTLADVGRRAOREFHGLGDCIITKIFKSGDLGLYGFNVSV 180
 DB 121 GAAGATSLCVYPLDFARTLADVGRRAOREFHGLGDCIITKIFKSGDLGLYGFNVSV 180
 OY 181 OGIIITRAAFVGYDPAKGLPDKNVHIFVSMIAQSVTAVALSLSPDYTRRRMMQ 240

DB 181 OGIIITRAAFVGYDPAKGLPDKNVHIFVSMIAQSVTAVALSLSPDYTRRRMMQ 240
 OY 241 SGRKGADIMYTGTVDCMRKIAKDEGAKAFKGAAMSNVLRMGCAFVLVLYDEIKKVV 297
 DB 241 SGRKGADIMYTGTVDCMRKIAKDEGAKAFKGAAMSNVLRMGCAFVLVLYDEIKKVV 297
 RESULT 4
 AAM61169
 ID AAM61169 standard; Protein; 298 AA.
 XX
 AC AAM61169;
 XX
 DT 28-SEP-1998 (first entry)
 XX
 DE Ant1 protein.
 XX
 KW Ant1; Adenine nucleotide translocator; cloning; screening;
 KW DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;
 KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
 KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
 KW lactic acidosis; degenerative muscle disease.
 XX
 OS Mus sp.
 XX
 PN WO9819714-A1.
 PD 14-MAY-1998.
 PF 31-OCT-1997; 97MO-US19882.
 PR 01-NOV-1996; 96US-0030017.
 PA (UYEM-) UNIV EMORY.
 PI Graham BC, Macgregor GR, Wallace DC;
 DR WPI: 1998-286608/25.
 DR N-PSDB: AAV36479.
 XX
 PT Mice lacking heart-muscle adenine nucleotide translocator protein -
 PT useful as model for mitochondrial myopathy and hypertrophic
 PT cardiomyopathy in animals and to test therapeutic compositions or
 PT gene therapies
 XX
 XX Disclosure; Page 39-40; 61pp; English.
 CC The present sequence is the mouse Ant1 protein, the cDNA producing this
 CC polypeptide is cloned by screening a mouse heart cDNA library with the
 CC human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA
 CC Tag dideoxy terminator cycle sequencing. The Ant1 protein is encoded by
 CC the Ant1 locus, a nuclear gene on chromosome 8. This protein is required
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
 CC which can then be converted into ATP. An Ant1 homozygous mutant would
 CC thus be defective in OXPHOS which results in disease in oxidative
 CC metabolism dependent tissues. This mouse Ant1 homozygous mutant can be
 CC used as a model system for fascioscapular humeral muscular dystrophy,
 CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
 CC systems can be used to test possible therapeutic compounds which
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
 CC independent of ANT1.
 XX
 SQ Sequence 298 AA:
 Query Match 93.9%; Score 1457.5; DB 19; Length 298;
 Best Local Similarity 93.6%; Pred. No. 5e-162;
 Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
 OY 1 MGHANSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASQISAEEKYKGIIDCVR 60
 DB 1 MGHANSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASQISAEEKYKGIIDCVR 60

QY 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDNRHKOFWRYFAGNLASG 120
 Db 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDNRHKOFWRYFAGNLASG 120
 QY 121 GAAGATSLCFYVPLDFARTRLAADYGR-AAOREFHGLDCLIKFKSGGLRGTYGFNV 179
 Db 121 GAAGATSLCFYVPLDFARTRLAADYGR-AAOREFHGLDCLIKFKSGGLRGTYGFNV 180
 QY 180 VGGIITVRAAFYGYVDTAKGMLPDPKNVHIFVSWMIASVAVAGLSYPTDVTARRMM 239
 Db 181 VGGIITVRAAFYGYVDTAKGMLPDPKNVHIFVSWMIASVAVAGLSYPTDVTARRMM 240
 QY 240 QSGRGADIMVTGYDVCWRKIAKDEGAKAFKFGAMSNVLRMGCAFVLVLYDEIKKY 297
 Db 241 QSGRGADIMVTGYDVCWRKIAKDEGAKAFKFGAMSNVLRMGCAFVLVLYDEIKKY 298

RESULT 5
 AA71032
 ID AA71032 standard; Protein: 298 AA.
 AC AA71032:
 XX 29-AUG-2000 (first entry)
 DE Human adenine nucleotide translocator ANT2.
 XX Human: adenine nucleotide translocator: ANT2; mitochondria; ADP: ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; nocotropic;
 KW antiparkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
 KW antiparkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 KW Homo sapiens.
 OS WO200026370-A2.
 XX 11-MAY-2000.
 PD 03-NOV-1999; 99WO-US25883.
 PF 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX (MITO-) MITOKOR.
 PA Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX WPI: 2000-365619/31.
 DR N-PSDB: AAD00520.
 XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX Claim 45; Page 172-173; 175pp; English.
 XX The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC d/ctri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated

CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 XX
 SO Sequence 298 AA;
 Query Match 89.6%; Score 1391.5; DB 21; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2,7e-154;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHMSFLKFLGAVAAVSKTAVAPIERVKLLQVHASKOISAEKQKGIIDCYVR 60
 Db 1 MTDALSFADKDFLAGVAAIASTKTAVERKLLQVHASKOITADKQKGIIDCYVR 60
 QY 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDNRHKOFWRYFAGNLASG 120
 Db 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDNRHKOFWRYFAGNLASG 120
 QY 121 GAAGATSLCFYVPLDFARTRLAADYGR-AAOREFHGLDCLIKFKSGGLRGTYGFNV 179
 Db 121 GAAGATSLCFYVPLDFARTRLAADYGR-AAOREFHGLDCLIKFKSGGLRGTYGFNV 180
 QY 180 VGGIITVRAAFYGYVDTAKGMLPDPKNVHIFVSWMIASVAVAGLSYPTDVTARRMM 239
 Db 181 VGGIITVRAAFYGYVDTAKGMLPDPKNVHIFVSWMIASVAVAGLSYPTDVTARRMM 240
 QY 240 QSGRGADIMVTGYDVCWRKIAKDEGAKAFKFGAMSNVLRMGCAFVLVLYDEIKKY 296
 Db 241 QSGRGADIMVTGYDVCWRKIAKDEGAKAFKFGAMSNVLRMGCAFVLVLYDEIKKY 297

RESULT 6
 AA001199
 ID AA001199 standard; Protein: 298 AA.
 AC AA001199:
 XX 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 XX Human: adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX Homo sapiens.
 OS WO200132876-A2.
 XX 10-MAY-2001.
 PD 03-NOV-2000; 2000WO-US30535.
 PF 03-NOV-1999; 99US-0434354.
 PR (MITO-) MITOKOR.
 PA Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelcebi G, Davis RE;
 XX WPI: 2001-291054/30.
 DR N-PSDB: AAS05902.
 XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX

PS Disclosure: Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-2
CC (ANT-2) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 298 AA;

Query Match 89.6%; Score 1391.5; DB 22; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.7e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDLFLAGAAVAAVSTAVAPIERVKLLLOVQHASKOISAEKQYGIIDCVVR 60
1 MTDAAISFAKDFLAGGAAVAAISKTAVAPIERVKLLLOVQHASKOITADKQYGIIDCVVR 60

OY 61 IPKEOGFLSWRGNLANVIRYPTQALNFAFKKQYKOLFLGVDKRFKQFRYFAGNLASG 120
61 IPKEOEVLSTWRGNLANVIRYPTQALNFAFKKQYKOLFLGVDKRFKQFRYFAGNLASG 120

OY 121 GAAGATSLCFVYPLDFARTLADVGR- AOREFHGLGDCIIRIFKSDJRGLYOGFNVS 179
121 GAAGATSLCFVYPLDFARTLADVGR- AOREFHGLGDCIIRIFKSDJRGLYOGFNVS 179

OY 180 VGGIIRYRAVFGVYDTAKMLDPKKNVHIFVSMIAQSVTAAVAGLSYDFDVRRRMM 239
180 VGGIIRYRAVFGVYDTAKMLDPKKNVHIFVSMIAQSVTAAVAGLSYDFDVRRRMM 239

OY 240 QSGRKGDIMYTGTLDCWKRIADDEGKAFKAGMSNVLRMGAGAPLVLYDEIKKY 296
241 QSGRKGDIMYTGTLDCWKRIADDEGKAFKAGMSNVLRMGAGAPLVLYDEIKKY 297

RESULT 7

AAU10379

ID AAU10379 standard; Protein: 298 AA.

AC AAU10379;

DT 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 2 (ANT2).

KW Human: adenine nucleotide translocator; ANT; ss;
KW mitochondrial matrix protein.

OS Homo sapiens.

PN WO200185944-A2.

PD 15-NOV-2001.

PF 11-MAY-2001; 2001WO-US15416.

PR 11-MAY-2000; 2000US-0569327.

PA (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
XX WPI: 2002-05598/07.
DR N-PSDB: AAS16689.

PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide

PS Claim 44; Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ADP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
XX The present sequence represents the amino acid sequence of human ANT2.

XX Sequence 298 AA;

Query Match 89.6%; Score 1391.5; DB 23; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.7e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDLFLAGAAVAAVSTAVAPIERVKLLLOVQHASKOISAEKQYGIIDCVVR 60
1 MTDAAISFAKDFLAGGAAVAAISKTAVAPIERVKLLLOVQHASKOITADKQYGIIDCVVR 60

OY 61 IPKEOGFLSWRGNLANVIRYPTQALNFAFKKQYKOLFLGVDKRFKQFRYFAGNLASG 120
61 IPKEOEVLSTWRGNLANVIRYPTQALNFAFKKQYKOLFLGVDKRFKQFRYFAGNLASG 120

OY 121 GAAGATSLCFVYPLDFARTLADVGR- AOREFHGLGDCIIRIFKSDJRGLYOGFNVS 179
121 GAAGATSLCFVYPLDFARTLADVGR- AOREFHGLGDCIIRIFKSDJRGLYOGFNVS 179

OY 180 VGGIIRYRAVFGVYDTAKMLDPKKNVHIFVSMIAQSVTAAVAGLSYDFDVRRRMM 239
181 VGGIIRYRAVFGVYDTAKMLDPKKNVHIFVSMIAQSVTAAVAGLSYDFDVRRRMM 240

OY 240 QSGRKGDIMYTGTLDCWKRIADDEGKAFKAGMSNVLRMGAGAPLVLYDEIKKY 296
241 QSGRKGDIMYTGTLDCWKRIADDEGKAFKAGMSNVLRMGAGAPLVLYDEIKKY 297

RESULT 8

AA71033

ID AA71033 standard; Protein: 298 AA.

AC AA71033;

DT 29-AUG-2000 (first entry)

DE Human adenine nucleotide translocator ANT3.

KW Human: adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; neurologic;
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200026370-A2.
 XX
 PD 11-MAY-2000.
 XX
 PE 03-NOV-1999; 99WO-US25883.
 XX
 PR 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clewenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 DR WPI: 2000-365619/31.
 DR N-PSDB; AAD00521.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 46; Page 173-174; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nucleic encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 CC
 XX
 SQ Sequence 298 AA;
 Query Match 89.2%; Score 1385.5; DB 21; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.4e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

DB 241 QSGRGADIMVTGYDCMRKIFRDEGKAFPKGAMSNVLRGMGAFVLYLDELKYY 298
 RESULT 9
 ID AAM39641
 XX AAM39641 standard; Protein; 298 AA.
 XX
 AC AAM39641;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2786.
 XX
 DE Human; nootropic; immunosuppressant; cytosolic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 KW
 XX Homo sapiens.
 OS
 XX
 XX WO200153312-A1.
 PN
 XX
 PD 26-JUL-2001.
 XX
 PE 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 23-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang Z, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou F, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB; AAI58797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 4; SEQ ID NO 2786; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 XX
 SQ Sequence 298 AA;
 Query Match 89.2%; Score 1385.5; DB 22; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.4e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.

Sequence 298 AA;
XX
XQ

SQ Sequence 298 AA;

Query Match	89.28; Score 1385.5; DB 23; Length 298,
-------------	---

Matches	260;	Conservative	21;	Mismatches	16;	Indels	1;	Gaps	1;
---------	------	--------------	-----	------------	-----	--------	----	------	----

QY	1	MGHANSFLKDELACGVAANAASKTVAIAIEVKKLLLOVHASAKOISEKKYKIIIDCVR	60
Db	1	MTKOALSPPKDELFIAGGIAAIAISKTVAIIEVKKLLLOVHASAKOIAADKQYKGIYDCIVR	60
QY	61	IPKEOGELAFSWGNLANVTRYPTPALNEAFKDKYKOLLFLGVDYRHKQEMFRYFAGLILASG	12
Db	61	IPKEOGELAFSWGNLANVTRYPTPALNEAFKDKYKOLLFLGVDYRHKQEMFRYFAGLILASG	12
QY	121	GAGGASLCEGVYPLDFAFRRLAANDGRR-AORENHGICDCLIKETFSDDLRLGLYQGFNS	17
Db	121	GAGGASLCEGVYPLDFAFRRLAANDGSKGSTRERERGLDCLVKTITSDGIRGLYQGFNS	18
QY	180	VGGIIITRYRAATFGVYDTAKGMLPDEKRNHIEVSMIAQSYTAAVAGLSTSEPTDVRRRMM	23
Db	181	VGGIIITRYRAATFGVYDTAKGMLPDEKRNHIVSMIAQSYTAAVAGVSYSEPTDVRRRMM	24
QY	240	QSGRKADIMTYGVYDCWKRILKDGCAKAFPKGAMSVNLKMGGAFAVLVLYDELIKKVV	297
Db	241	QSGRKADIMTYGVYDCWKRILFRODGGGAFFPKGAMSVNLKMGGAFAVLVLYDELKKVI	298

RESULT 12
AAM41427

AC AAM41427;

DT 22-OCT-2001 (first entry)

DE	Human polypeptide	SEQ ID NO	6358

KM Human; immunosuppressant; cytostatic; gene therapy; cancer
KM peripheral nervous system; neuropathy; central nervous system; CNS;
KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KM chemokilnetic; thrombolytic; drug screening; arthritis; inflammation;
KM leukaemia.

OS Homo sapiens.

PN WO200153312-A1

PD 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

PR 21-JAN-2000; 2000US-0488725

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312
PR 03-AUG-2000; 2000US-0653450
PR 14-SEP-2000; 2000US-0662191
PR 19-OCT-2000; 2000US-0693036
PR 29-NOV-2000; 2000US-0727344

PA (HYSE-) HYSEQ INC

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac R;

DR WPI; 2001-442253/47.
DR N-PSDB; AAI60583.

PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

PS Example 2; SEQ ID NO 6358; 10078bp; English.

CC The invention relates to human nucleic acids (AM157798-AM161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

SQ Sequence 323 AA;

SQ Sequence 323 AA;

Query Match 89.28; Score 1385.5; DB 22; Length 323;

Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY	1	MGAMSGELKQFLAGAAVAAASKTAAVPIEYVKLLILOYHAKSIOISAEKQYKGIIDCVR	60
QY	26	MTEDQISAPKDFLGGIILAAISKTAAVAETEKVKLLILOYHAKSIOIADKQYKGIIDCVIR	85
Db	61	IPKEGGLSEPMRGMLANVIYRFTPTQALNFARKDKYKQLELGGVDRHMQFWREYFAGNLASG	120
QY	86	IPKEGGLSEPMRGMLANVIYRFTPTQALNFARKDKYKQLELGGVDRHMQFWREYFAGNLASG	145
Db	121	GAAGATSLCFYYPILDFEARTRLAADYGR - AOREFHGLGDLCTIKTFKSDGLRGLYQGSNVS	175
QY	146	GAAGATSLCFYYPILDFEARTRLAADYGVGSGTIERERGLGDLCTIKTFKSDGILGLYQGSNVS	205
Db	180	VQGIITTYFAAFYGVYDTRKGLMPRKNVHIVFSNMIIQASVYAVAGLSLSEPDYVRRRMM	235
QY	206	VQGIITTYFAAFYGVYDTRKGLMPRKNVHIVFSNMIIQATYAVAGVSYSPEDYVRRRMM	265
Db	240	QSGRRGADIMYTGIVDCMRKITAQDEGAKAFKFGKAMSVNLRGMGAFVLVLYDEITKKYV	297
QY	266	QSGRRGADIMYTGIVDCMRKITAQDEGAKAFKFGKAMSVNLRGMGAFVLVLYDEITKKYV	323

RESULT 13

ID ABG15423 standard; Protein; 325 AA.

AC ABG15423

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #15414

```
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW Food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
PI WPI: 2001-639362/73.
XX
DR N-PSDB; AAS79610.
XX
DR
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 45782; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (I.). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABB00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 325 AA:
Query Match 83.4%; Score 1294.5; DB 22; Length 325;
Best Local Similarity 83.4%; Pred. No. 7.3e-143;
Matches 251; Conservative 19; Mismatches 26; Indels 5; Gaps 4;
```

```
OY 237 MMQSGRKADIMTGTVDCKRIAKDEGAKAFKGCAMSVLRGCGAFVLVYD-EIRK 295
DB 264 EXMOSGRKGDIMYTGTLDCKRRIARDEGKAFKGCAMSVLRGCGAFVLVYEXSKK 323
OY 296 Y 296
DB 324 Y 324
RESULT 14
ABB66082
ID ABB66082 standard; Protein; 299 AA.
AC ABB66082;
DE 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 25038.
XX Drosophila: developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX Drosophila melanogaster.
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PMD, Myers EW;
XX
DR WPI: 2001-656860/75.
XX
DR N-PSDB; ABL10185.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 25038; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences and pharmaceutical drugs. The invention
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (AB57737-AB872072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 299 AA:
Query Match 79.9%; Score 1241; DB 22; Length 299;
Best Local Similarity 79.7%; Pred. No. 1.2e-136;
Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;
```

Db 127 ATSLCFVYPLDFAPNTRLAADYDGRKGQGHFFLGLNCLIRKSDSDIVGLYKGFVSGIIT 166
 |||||
 Qy 185 IYRAAYFGVYDTAKGMLPDKPNVHI EYVSMIAQSVYAVAGLLSTP EDTVRRRMMSGRK 244
 |||||
 Db 187 IYRAAYFGFYDTAGKMLPDKPNTRIYISMAIAQVYTVAGIVSYSPEDTVRRRMMSGRK 246
 |||||
 Qy 245 GADIMYDTYDVCWRRKIAKDECAKAFKFGAGSNVYLRGSGAVLYLXDYEIRK 295
 :|||
 Db 247 ATEVIYKNTLLHCMAPIIAKQDSGTAFEGKASNNILRGAGAVLYLXDYEIRK 297
 |||||

RESULT 15
ABB67300

AC ABB67300;

DT 26-MAR-2002 (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 28692.

KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

05 *Drosophila melanogaster*

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

XX
XX

XX

XX

DR N-PSDB; ABL11403.

PT New isolated nucleic

PT interactions -

PS Disclosure; SEQ ID NO 28692; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent

CC useful in developmental biology and in elucidating cell signalling and CC cell-cell interactions in higher organisms for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC disclosed a novel DNA sequence (APR16176-APR30511) associated with

CC sequences (ABL01840-ABL161/5) and the encoded proteins (ABP5737-ABP73073)

CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in a separate format directly from WRC

CC at http://www.wipo.int/patent_sequences.

SQ	Sequence	299 AA;
----	----------	---------

Query Match	79.98;	Score 1241;	DB 22;	Length 299;
Post Local Client	70.78;	Score 1241;	DB 22;	Length 299;

Matches	232;	Conservative	26;	Mismatches	33;	Indels	0;	Gaps	0;
---------	------	--------------	-----	------------	-----	--------	----	------	----

QY 5 AWSFLKDFLAGAVAAAVSKTAVAPIERVKLLQVQHASKQISAEEKYKGIIDCVRIKPE 64

Db 7 AVGVKDEAAGCISA AVSKTAVAPIERVKLLQVQHISKQISPDKQYKGMVDCFIRIPKE 66

65 QGFLSFWRGNLAVIRYPTQALNEAFKDKYKQLFLGGVDRHKQFWRYFAGNLSGGAAG 12

Db 67 QGFSSFMKGNLANVIRFPPQALNFARKDKYKQVFLGGVADKNQFMWRYFAGNLANSGAAG 126

Qy 125 ATSLCEVYPLDFPARTRLADYGRRAQREPHGLGDCIIKFSQDLKGLYQGFENVSVQGIT 184

Db 127 ATSLCEVYPLDFPARTRLAADYGRKGGQREPHGLGNCILTKIKFSQDGLYGLRGFENVSVQGIT 186

Qy 185 IYRAAYFQVYDTARGMLPDRKNVNIIFVSMIAQSVYAVAGLLSPFPTVRRRMMSGRK 244

Db 187 IYRAAYFQVYDTARGMLPDRKNVNIIFVSMIAQSVYAVAGIVSPFPTVRRRMMSGRK 246

Qy 245 GADINVTCTVDQMRRIKADDEGAKAFKFGAANSVYLRGMSGAFVLYLDEIKK 295

Db 247 ATEVYIKKTLTLCMATIAKQEBTGAFKFGAANSVYLRGMSGAFVLYLDEIKK 297

Search completed: November 12, 2002, 16:45:56
Job time : 30.9328 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:25 : Search time 11.6405 Seconds
(without alignments)
750.705 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGVA...LNGMGAFVLYDEIKKV 297

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/6CTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/6ackfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1457.5	93.9	298	3	US-08-961-871-10 Sequence 10, App1
2	301	19.4	469	4	US-09-188-930-339 Sequence 339, App
3	291	18.7	447	4	US-09-160-119-4 Sequence 4, App1
4	291	18.7	674	4	US-09-160-119-2 Sequence 2, App1
5	267	17.2	291	4	US-09-501-558-2 Sequence 2, App1
6	238	15.3	320	2	US-08-933-750C-12 Sequence 12, App1
7	238	15.3	320	4	US-09-234-613-12 Sequence 12, App1
8	233.5	15.0	299	1	US-08-518-878B-56 Sequence 56, App1
9	227	14.6	299	1	US-08-470-868A-56 Sequence 56, App1
10	227	14.6	309	1	US-08-518-878B-51 Sequence 51, App1
11	227	14.6	309	2	US-08-807-861A-51 Sequence 51, App1
12	227	14.6	309	2	US-08-470-868A-51 Sequence 51, App1
13	227	14.6	309	3	US-09-681-51 Sequence 51, App1
14	227	14.6	309	3	US-08-946-719A-51 Sequence 51, App1
15	227	14.6	311	2	US-08-775-009-33 Sequence 33, App1
16	227	14.6	311	2	US-08-775-009-32 Sequence 32, App1
17	225	14.5	308	2	US-08-937-466-2 Sequence 2, App1
18	222.5	14.3	308	2	US-09-172-528-2 Sequence 2, App1
19	222.5	14.3	308	3	US-09-318-199-2 Sequence 2, App1
20	222.5	14.3	308	3	US-09-503-579-2 Sequence 2, App1
21	218.5	14.1	432	2	US-08-937-466-4 Sequence 4, App1
22	218.5	14.1	432	2	US-09-172-528-4 Sequence 4, App1
23	218.5	14.1	432	3	US-09-318-199-4 Sequence 4, App1
24	218.5	14.1	432	4	US-09-503-579-4 Sequence 4, App1
25	208.5	13.4	293	4	US-09-501-558-4 Sequence 4, App1
26	208.5	13.4	307	2	US-08-807-861A-56 Sequence 56, App1
27	196.5	12.7			

28	196.5	12.7	307	3	US-09-210-681-56 Sequence 56, App1
29	196.5	12.7	307	3	US-08-946-719A-56 Sequence 56, App1
30	193	12.4	303	1	US-08-294-522B-36 Sequence 36, App1
31	192	12.4	303	1	US-08-518-878B-37 Sequence 37, App1
32	192	12.4	303	2	US-08-807-861A-37 Sequence 37, App1
33	192	12.4	303	2	US-08-470-868A-37 Sequence 37, App1
34	192	12.4	303	3	US-09-210-681-37 Sequence 37, App1
35	192	12.4	303	3	US-08-946-719A-37 Sequence 37, App1
36	190.5	12.3	306	5	PCT-US94-09799-1 Sequence 1, App1
37	188.5	12.1	351	2	US-08-933-750C-19 Sequence 19, App1
38	188.5	12.1	351	4	US-09-234-613-19 Sequence 19, App1
39	185.5	11.9	328	4	US-09-068-140A-15 Sequence 15, App1
40	176	11.3	256	2	US-08-937-466-6 Sequence 6, App1
41	176	11.3	256	2	US-09-172-528-6 Sequence 6, App1
42	176	11.3	256	3	US-09-318-199-6 Sequence 6, App1
43	176	11.3	256	4	US-09-503-579-6 Sequence 6, App1
44	176	11.3	312	4	US-09-188-930-142 Sequence 142, App
45	175.5	11.3	289	4	US-09-068-140A-10 Sequence 10, App1

ALIGNMENTS

RESULT 1
US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Macgregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10
Query Match 93.9%; Score 1457.5; DB 3; Length 298;
Best Local Similarity 93.6%; Pred. No. 4.1e-161;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
QY 1 MGDHMSFLKDFLAGVA...LNGMGAFVLYDEIKKV 60

```
Db 1 MGDDALSLKDFLAGGIAAASKTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVR 60
OY 1PKREGFLSPFRGNLANVIRFPTQALNFAFKDKYKOLFGLGVBHKKOFMYEPAGNLASG 120
Db 61 IPKREGFLSPFRGNLANVIRFPTQALNFAFKDKYKOLFGLGVBHKKOFMYEPAGNLASG 120
OY 121 GAAGATSLCFYPLDFPARTLADVGR-RAOREFHGLDCCIIRKIFKSDGLRGLYOGFVNS 179
Db 121 GAAGATSLCFYPLDFPARTLADVGR-RAOREFHGLDCCIIRKIFKSDGLRGLYOGFVNS 180
OY 180 VOGIITIAAATFVYDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSTPFDYVRRMM 239
Db 181 VOGIITIAAATFVYDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSTPFDYVRRMM 240
OY 240 QSGRKADIMVTGVDCAKRIAKDEGAKAFKGSAMSVNLRGMGAFVLYLDEIKKYV 297
Db 241 QSGRKADIMVTGVDCAKRIAKDEGAKAFKGSAMSVNLRGMGAFVLYLDEIKKYV 298
```

```
RESULT 2
US-09-188-930-339
; Sequence 339, Application US/09188930A
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-339
```

Query Match 19.4%; Score 301; DB 4; Length 469;
Best Local Similarity 28.9%; Pred. No. 2.4e-26;
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;

```
OY 6 WSFLKDFLAGVAAVSTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVR-RI 61
Db 187 WRHL--VAGGAGAVSTCTAIPDLRLKVLMOV-HASRNNM-----CIYGGFTQM 233
OY 62 PKEOGFLSPFRGNLANVIRFPTQALNFAFKDKYKOLFGLGVDR---HKOFMYEPAGN 116
Db 234 IREGGAKSLMGNGINIVKIPESAIKFMAYEQMKRLV--GSDQETLRIHER----- 283
OY 117 LASGAGATSLCFYPLDFPARTLADVGRRAOREFHGLDCCIIRKIFKSDGLRGLYOGF 176
Db 284 LVASLSLGAIAOSSIIYPMIEVLKTRMAL---RKTGOYSGMLDCARRILAKGVAFAFKGY 339
OY 177 NVSVOGIITIAAATFVYDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSTPFDYVRRMM 227
Db 340 IPNMIGIITPYGIDLAIVETELKTNWLOKRYAVNSAP--GVFV-LLAGGTISTTCGOIAS 395
OY 228 YPFDVRRMMQSGRKADIMVTGVDCAKRIAKDEGAKAFKGSAMSVNLRGMGAFV- 286
Db 396 YPLALVTRRMQAQASIEGAPEVTMSL--FKQILRTBGAFGLRGLAPNPKVIPAISVS 453
OY 287 LVLYDEIK 294
Db 454 YVYVENLK 461
```

RESULT 3

```
US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-4
```

Query Match 18.7%; Score 291; DB 4; Length 447;
Best Local Similarity 27.5%; Pred. No. 3.2e-25;
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;

```
OY 12 FLAGVAAVSTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVRIPKREGFLSPFW 71
Db 104 FGLSSVAGAVATAVYPLDLVKTMMONORSTGVSFVGLMTKNSDCKRKVIRYGGFGLY 163
OY 72 RGNLANVIRFPTQALNFAFKDKYKOLFGLGVDRHKKOFMYEPAGNLASGAAGATSLCFV 131
Db 164 RGLLPQLGLVAPKAIKLTVDNDFRDKFM----HKGSVPLAEAILLAGCAGGSQYIFT 218
OY 132 YPLDFARTRL--AADV--GRAQREFHGLDCCIIRKIFKSDGLRGLYOGFVNSVOGIITIR 187
Db 219 NPLEIVKIRILOVAGEIITTPRVS-----ALSVARDLGFPGIYKAKACFLRDI PFS 269
OY 188 AAFVGVYDTAKGMLPDPKNVHIFVSMIAOSVAV-AGLISYPPDVTYVRRMMQSGRGA 246
Db 270 AIFPCVIAHVKASFRANEGOVSPGSLLAGAIAGPAAISLVTPADYIKTR--LOYAARAG 327
OY 247 DIMYGTVDCAKRIAKDEGAKAFKGSAMSVNLRGMG-APVLYLYDEIKKY 296
Db 328 QTTYSGVIDCFRKILREGGPKALMKAGARVRSPPQGVLYLLTYELLQRW 378
```

```
RESULT 4
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-2
```

Query Match 18.7%; Score 291; DB 4; Length 674;

[illegible]

```

RESULT 5
US-09-558-2
: Sequence 2, Application US/09501558
: Patent No. 6403784
: GENERAL INFORMATION:
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Mathur, Brian
: APPLICANT: Zambrowicz, Brian
: APPLICANT: Sands, Arthur T.
: TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
: FILE REFERENCE: Lex-0012-USA
: CURRENT APPLICATION NUMBER: US/09/501,558
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 291
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-501-558-2

Query Match      17.2%; Score 267; DB 4; Length 291;
Best Local Similarity 28.4%; Pred. No. 1e-22;
Matches 84; Conservative 51; Mismatches 137; Indels 24; Gaps 9;

QY 10 KDLFAGVAVAAVSTAAVPIERVKLLDVOVHASKDIS-AEKQYKGIICVVRIPKEQFL 68
   | : : : : : | : | : | : | : | : : | : | : | : | : | : | : |
Db 7 KPFYVGGASLTAEGGTFPIDLTKTRLDIQOGOTNDARKFKEIRROMLALVRIQEGEGLK 66

QY 69 SFHGNLANLVRIPTQALNFAFKDKYKQLELGCYDRHKQEMRYPAGNLASGAAGATSL 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 ALYSGIAPAMLRQASVYGTIKIGTYQSLKRLF--IERPED--ETLPVIVIGSILSGVTS 121

QY 129 CFVVPDLFAPTRLADADVGRRAQREFHGGDDCIKIFKSDGLRGIVQGFVSVQGIITYRA 188
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 TIANPTDVLKLRMQA----QSNTIQGGAIHGFNMNIYQOEGTRGLMKVSLTRQRAIYVG 177

QY 189 AYFGVYDTAK-----GMLDPKKNVHIFVSMIAQSVTAVAG-LLSYPDFVTRRRMQOS 241
   | : | : | : | : : : : : : : : : : : : : : : : : : : : : :
Db 178 VELPVYDITTKHLLISGLMGDVTYVTHLSF-----TCGLGALALNSVPDVTTRMMNQR 232

QY 242 G-RKGADIMYGTGVDCMKRIAKDEGAKAFKFGAWSNVLK-GMGAGFVLYLDEIKK 295
   | | | | | | | | | | : | : | : | : | : | : | : | : | : |
Db 233 VLRGRCRGSGYGTLDCLLTQTKWKNESGFALYRGFMFMNLRLGPMNIIFVYTYEQLRK 288

RESULT 6
US-08-933-750C-12

```

```

1 Sequence 12 Application US/08933750C
2 Patent No. 5932442
3
4 GENERAL INFORMATION:
5 APPLICANT: Lal, Preeti
6 APPLICANT: Hillman, Jennifer L.
7 APPLICANT: Bandman, Olga
8 APPLICANT: Shah, Purvi
9 APPLICANT: Au-Young, Janice
10 APPLICANT: Yue, Henry
11 APPLICANT: Guegler, Karl J.
12 APPLICANT: Corley, Neil C.
13 TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
14 NUMBER OF SEQUENCES: 98
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE: Incyte Pharmaceuticals, Inc.
17 STREET: 3174 Porter Drive
18 CITY: Palo Alto
19 STATE: CA
20 COUNTRY: USA
21 ZIP: 94304
22
23 COMPUTER READABLE FORM:
24 MEDIUM TYPE: Diskette
25 COMPUTER: IBM Compatible
26 OPERATING SYSTEM: DOS
27 SOFTWARE: FASTSEQ for Windows Version 2.0
28 CURRENT APPLICATION DATA:
29 APPLICATION NUMBER: US/08/933.750C
30 FILING DATE: September 23, 1997
31 CLASSIFICATION: 536
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER:
34 FILING DATE:
35 ATTORNEY/AGENT INFORMATION:
36 NAME: Billings, Lucy J.
37 REGISTRATION NUMBER: 36,749
38 REFERENCE/DOCKET NUMBER: PF-0356 US
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: 415-855-0555
41 TELEFAX: 415-845-4166
42 TELEX:
43
44 INFORMATION FOR SEQ ID NO: 12:
45 SEQUENCE CHARACTERISTICS:
46 LENGTH: 320 amino acids
47 TYPE: amino acid
48 STRANDEDNESS: single
49 TOPOLOGY: linear
50 IMMEDIATE SOURCE:
51 LIBRARY: SPLNNOT02
52 CLONE: 207452
53
54 US-08-933-750C-12

```

[illegible]

Db 243 RLQVGFEHARAAGVRRYKGLMDCAKOVLOKRGALGFFKGLSPSLIKALSTGFMFFS 302
QY 290 YD 291
Db 303 YE 304

RESULT 7

US-09-234-613-12
; Sequence 12, Application US/09234613
; Patent No. 6132973
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Puri
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,613
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SPLN0702
; CLONE: 207452
; US-09-234-613-12

Query Match 15.3%; Score 238; DB 4; Length 320;
Best Local Similarity 23.5%; Pred. No. 2.8e-19;
Matches 71; Conservative 67; Mismatches 124; Indels 40; Gaps 10;

QY 13 LAGAVAAVSTAVAPIRKVLLOVHAS-KQISAEOYGIIDCVVIRKREGFLSFW 71
Db 20 VAGSVGLVTRALISPFVIRKIROHERLSRSDPSAKYGIIOASROILOEGEPFAFW 79
QY 72 RGNLANVIRYPTQALN-AFKDKYKOLFGLGVDRHKQFWRYPFAGNLASGAAGTSLCF 130
Db 80 KGHVPAQILSLIGYVQFLSTBMLTELVHRSSVDAREFSVHF---VCGGLACMAVLT 135
QY 131 VPLDFARTRLADVGRRAOREFHGLGDCIIRKSDGLRGLYGFNVSVGGIITRYAAV 190

Db 136 VHPVDVLTREAA---QGEPRVYNTLRHNAVGTMYRSEGPQVYKGLAPTLIAIPYAGLQ 192
QY 191 FGVDYTKAGMLPDPKKNHIEFYSMMI-----AOSTAVAGLLSYFEDTVRR 235
Db 193 FSCYSILK-----HLV-KWAIPEAGKKNENIQLGSGAGVSKTLYPLDLFKK 242
QY 236 RMM---OSGRK--GADIMTGTVDCKRKIKADEGAKAFPGKANSVLR-GMGAPVLYL 289
Db 243 RLQVGFEHARAAGVRRYKGLMDCAKOVLOKRGALGFFKGLSPSLIKALSTGFMFFS 302
QY 290 YD 291
Db 303 YE 304

RESULT 8

US-09-142-565-2
; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; US-09-142-565-2

Query Match 15.0%; Score 233.5; DB 4; Length 312;
Best Local Similarity 24.7%; Pred. No. 9e-19;
Matches 73; Conservative 53; Mismatches 145; Indels 25; Gaps 8;

QY 12 FLAGVAAVSTAVAPIRKVLLOVHAS-KQISAER--QYKGIIDCVVIRKREGFLS 69
Db 17 FLGAGTACCFADLVTFPLDTAKVRLIOGENQAVOTARLVQYRGVLTITLVRTGSPCS 76
QY 70 FWRGNLANVIRYPTQALNFAFKYKOLF-GGVDRHKQFWRYPFAGNLASGAAGTSL 128
Db 77 PYNGLVAGLQROMSFASIRIGLYSVKQYTPRKADNSLTRLILA-----GCTTGAAV 131
QY 129 CFVYPLDFARTRLADV---GRRAREFHGLGDCIIRKSDGLRGLYGFNVSVGGIIT 185
Db 132 TCAQPTDVAVKVFQASHLGPSSDRKYSTMDAYRTIAREGVRLGKGLPIMINRAI 191
QY 186 YRAAFVGYDTPAKGMLPDPKKNHIEFVSMTAOSTA-----VAGLLSYFEDTVRRMMQ 240
Db 192 VNCAEVYVYDILKRLID--YHLITDNFPCHFVSARGAGCAVVASPVDDVYTRYM-- 246
QY 241 SGRGADIMTGTVDCKRKIKADEGAKAFPGKANSVLR-GMGAPVLYLDEIKK 295
Db 247 ---NSPEQVTSPLDCMIKMWAOBEPYAFYGFPSFLRLGSMNVVMVYIEOLKR 299

RESULT 9

US-08-518-878B-56
; Sequence 56, Application US/08518878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-56

Query Match 14.6%; Score 227; DB 1; Length 299;
Best Local Similarity 23.8%; Pred. No. 4,8e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

QY 12 FLAGAANAASKTAVAPIERKLLLOVHASK--QISAEKOYGIIDCVRIPIKQGF 68
DB 7 FLGAGTAACIADLITPELPDTAKVRLQIGESQGPVATSAQYRGVWGTLTIVRTGPR 66
QY 69 SFRGMLANVIRFPFOALNFAKDKYKQLFLGCVNRHKOFRYFNGNLASGAACATSL 128
DB 67 SLVNGVLAVGLOROMSPASVRIGLYDSVKOFTYKSGSHAS----IGSRLLAGSTGALAV 121
QY 129 CFVYPLDFATRIADVGRRAQREFHGLDCIIFKSDGLRGLYGFNVSGIITRYA 188
DB 122 AVAAPTVDVAVKVRQAOARAGGRRYQSTVNAVYTIAREGFRGLMKGTSPNARNAIUNC 181
QY 189 AFGVYDTAK-----GMLDPKKNVHIFVSMIAQSVTAVAGLLSPFTVRRMMQSG 242
DB 182 AELVTYDLIKDALILKANLMTDLPCH-FTSAGFAGCTTV---IASPVDVVKTRYM---- 233
QY 243 RKGAADIMYGTVCWKRKIAKDEGAKAFPGAMSNVLR-GMGAFVLYLDEIK 295
DB 234 -NSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSLRLGSMNVVMFVTEQLKR 286

RESULT 10
US-08-470-868A-56
Sequence 56, Application US/08470868A
Patent No. 5661485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-56

Query Match 14.6%; Score 227; DB 2; Length 299;
Best Local Similarity 23.8%; Pred. No. 4,8e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

QY 12 FLAGAANAASKTAVAPIERKLLLOVHASK--QISAEKOYGIIDCVRIPIKQGF 68
DB 7 FLGAGTAACIADLITPELPDTAKVRLQIGESQGPVATSAQYRGVWGTLTIVRTGPR 66
QY 69 SFRGMLANVIRFPFOALNFAKDKYKQLFLGCVNRHKOFRYFNGNLASGAACATSL 128
DB 67 SLVNGVLAVGLOROMSPASVRIGLYDSVKOFTYKSGSHAS----IGSRLLAGSTGALAV 121
QY 129 CFVYPLDFATRIADVGRRAQREFHGLDCIIFKSDGLRGLYGFNVSGIITRYA 188
DB 122 AVAAPTVDVAVKVRQAOARAGGRRYQSTVNAVYTIAREGFRGLMKGTSPNARNAIUNC 181
QY 189 AFGVYDTAK-----GMLDPKKNVHIFVSMIAQSVTAVAGLLSPFTVRRMMQSG 242
DB 182 AELVTYDLIKDALILKANLMTDLPCH-FTSAGFAGCTTV---IASPVDVVKTRYM---- 233
QY 243 RKGAADIMYGTVCWKRKIAKDEGAKAFPGAMSNVLR-GMGAFVLYLDEIK 295
DB 234 -NSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSLRLGSMNVVMFVTEQLKR 286

RESULT 11
US-08-518-878B-51
Sequence 51, Application US/08518878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 12
US-08-807-861A-51
Sequence 51, Application US/08807861A
Patent No. 5853975
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TREATMENT OF OBESITY
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878

RESULT 13
 US-08-470-868A-51
 ; Sequence 51, Application US/08470868A
 ; Patent No. 5861485
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis C.
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie and Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,868A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.

```

: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7853-0031-9999
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-8864
:
: TELE: 66441 PENNIE
:
: INFORMATION FOR SEQ ID NO: 51:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 309 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
:
: TOPOLOGY: unknown
:
: OS-08-470-868A-51

```

Query Match	14.6%;	Score 227;	DB 2;	Length 309;
Best Local Similarity	23.8%;	Pred. No. 5e-18;		
Matches 70;	Conservative 52;	Mismatches 148;	Indels 24;	Gaps 77;

Qy	12	FLAFAVAAAASKTVAPLIERKLLLOVQAHSK---QJSAEKQKGIIDCVARJPEKGGFL	68
Db	17	FLAGAGTAACIADLITFPDLTRAKVRLQIQEGSQGVRKATVSAQIRGVNGVITLTMTKTEGPR	76
Qy	69	SEWRGNLANVIRFPYQALNFAFKDKYKQLFLGVDNRHKQFWRYFACNIALSGAAGATSL	128
Db	77	SLYNGTLVAGLQROMSFASVIRIGLVDYSVKQFYTKGSEHAS-----IGSRLLAGSPITGLAV	131
Qy	129	CFVYFLDFAFRRLADVGRRAQREFHGLDGIIRKFSDDLRLGLQGFNFNVSGGIIYYRA	188
Db	132	AVAAOPTVVKVRFQQAQAPAGCGRRYQSTVNAAYKTTIAEEEGSRGLMKTSPNVAATAVNC	191
Qy	189	AYFGVDYTAQ-----QMLDPKPVNHIFFVSNMIAQSYTAAGAGLSTYEPDVFVRRRMQSG	242
Db	192	AELVTYDILKIDALLKANLMTDPLCH-FTSAFGAGFCTTV---IASVDVAVKTRPYM----	243
Qy	243	RKGADIMTYGVDGCKRIADDEGAKAFPKGMSNVLR-GMGAGFVLYLJDEIKR	295
Db	244	-NSALGQYSSAGHCALMTMLRKEGGRABYKKGMPSEFLGLGSSNVNVMFTYTDLKR	296

RESULT 14
 US-09-210-681-51
 : Sequence 51, Application US/09210681
 : Patent No. 6057109
 :
 : GENERAL INFORMATION:
 : APPLICANT: Tartaglia, Louis A.
 : TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 : TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 :
 : NUMBER OF SEQUENCES: 64
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Penile & Edmonds LLP
 : STREET: 1155 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 10036-2711
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/210,681
 : FILING DATE:
 : CLASSIFICATION:
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/807,861
 : FILING DATE: 26-FEB-1997
 : APPLICATION NUMBER: US 08/518,878
 : FILING DATE: 23-AUG-1995
 : APPLICATION NUMBER: US 08/470,868
 : FILING DATE: 06-JUN-1995
 : APPLICATION NUMBER: US 08/294,522
 : FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-09-210-681-51

Query Match	14.68;	Score 227;	DB 3;	Length 309;
Best Local Similarity	23.88;	Pred. No. 5e-18;		
Matches 70;	Conservative 52;	Mismatches 148;	Indels 24;	Gaps 77;

Qy	12	FLAGVAAAVASTAAPLIERVYKLLLOVONJASK----	OISEKYOYKGIIDCVIRPKROGL	68
Db	17	FLGAGTAAACIADLIFEPDLDTAKVRKQIQGESGSPPARATYSADYRGVMGIIILMVRREGRR		76
Qy	69	SFWRCNLANVIRYFPTQALNFAFKDKYKQLETGVDNRHKQFMRVYFAGNVLASGGAAGATSL		128
Db	77	SLYNGLVAGLOROMSPFASVIRIGLYSVSKQFYTKGSEHAS----	IGSRLLASTGTALAY	131
Qy	129	CFVYVLDGARPTFLADVGRADREPHGJGDCILIKIFKSGDLRGLYGVFNVSOGIITVYA		188
Db	132	AAVAQPTDVVKKRFQOARAGGGRKYOSTYVNAKKTJAREGEFGMLMGISPNVARNALIVNC		191
Qy	189	AYFGVYDTAK-----GMLPDKNVHIFVSNMIAOSVTVAÄLLSYFEDTVERRMMOSG		242
Db	192	AEIYVYDILIKDALLKANILMTDLPCH-FTSAGAGACTTJ-----IASPVDVVKTRYA----		243
Qy	243	RKGALIMTGVYDCKRKITAKDGAANAFTFGANSNVLR-CMGCAFVLYLYLDELKK		295
Db	244	NSALGQVYSAGACHALTMLOKEGPRAFYVGGFMSPLRLGSMNVNVMVEYTEQLK		296

RESULT 15
 US-08-946-719A-51
 : Sequence 51 Application US/08946719A
 : Patent No. 6121017
 : GENERAL INFORMATION:
 : APPLICANT: Tartaglia, Louis A.
 : TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 : TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 : NUMBER OF SEQUENCES: 64
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Pennie & Edmonds LLP
 : STREET: 1155 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 10036-2711
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/946,719A
 : FILING DATE: 8-OCT-1997
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/807,861
 : FILING DATE: 26-FEB-1997
 : APPLICATION NUMBER: US 08/518,878
 : FILING DATE: 23-AUG-1995
 : APPLICATION NUMBER: US 08/470,868
 : FILING DATE: 06-JUN-1995

QY 181 GGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSTPFTVRRMMQ 240
 |||||
 Db 181 GGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSTPFTVRRMMQ 240
 QY 241 SGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYV 297
 |||||
 Db 241 SGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYV 297

RESULT 2

US-09-810-644-31
 ; Sequence 31, Application US/09810644
 ; Patent No. US20020012992A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Willey, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pel, Yezhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D3
 ; CURRENT APPLICATION NUMBER: US/09/810,644
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 297
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-810-644-31

Query Match 100.0%; Score 1553; DB 10; Length 297;
 Best Local Similarity 100.0%; Pred. No. 1.9e-154;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHAWSLFKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 |||||
 Db 1 MGDHAWSLFKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 QY 61 IPKDEGLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHGFWRFPAGNLASG 120
 |||||
 Db 61 IPKDEGLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHGFWRFPAGNLASG 120
 QY 121 GAAGATSLCFEYYPIDFARTRLADVGRRARERFGLGDCIIRKFSDDLRLGLYOGFNVS 180
 |||||
 Db 121 GAAGATSLCFEYYPIDFARTRLADVGRRARERFGLGDCIIRKFSDDLRLGLYOGFNVS 180
 QY 181 GGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSTPFTVRRMMQ 240
 |||||
 Db 181 GGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSTPFTVRRMMQ 240
 QY 241 SGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYV 297
 |||||
 Db 241 SGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKYV 297

RESULT 3

US-09-811-094-32
 ; Sequence 32, Application US/09811094
 ; Patent No. US20010044144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Willey, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.

; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pel, Yezhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D4
 ; CURRENT APPLICATION NUMBER: US/09/811,094
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-811-094-32

Query Match 89.6%; Score 1391.5; DB 10; Length 298;
 Best Local Similarity 88.6%; Pred. No. 1.3e-137;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHAWSLFKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 |||||
 Db 1 MGDHAWSLFKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 QY 61 IPKDEGLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHGFWRFPAGNLASG 120
 |||||
 Db 61 IPKDEGLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHGFWRFPAGNLASG 120
 QY 121 GAAGATSLCFEYYPIDFARTRLADVGRRARERFGLGDCIIRKFSDDLRLGLYOGFNVS 179
 |||||
 Db 121 GAAGATSLCFEYYPIDFARTRLADVGRRARERFGLGDCIIRKFSDDLRLGLYOGFNVS 180
 QY 180 VGGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSTPFTVRRMMQ 239
 |||||
 Db 180 VGGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSTPFTVRRMMQ 240
 QY 240 QSGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKY 296
 |||||
 Db 240 QSGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNVLRGMGAFVLYLDEIKKY 297

RESULT 4

US-09-810-644-32
 ; Sequence 32, Application US/09810644
 ; Patent No. US20020012992A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Willey, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pel, Yezhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D3
 ; CURRENT APPLICATION NUMBER: US/09/810,644
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-810-644-32

Query Match 89.6%; Score 1391.5; DB 10; Length 298;
 Best Local Similarity 88.6%; Pred. No. 1.3e-137;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHAWSLFKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60

Db	1	MTDALSFARKPFLAGGAAAIASKTAAPVPIERVKLLLOVHASAKOITADKOYKGIITDCVRR	60
Oy	61	IPKROGFLSPMRGRLANVIRFFPQALNPAFKDXYKQLPLGAGVDRHNOFMRYFAGNLASG	120
Db	61	IPKROEVLSPMRGRLANVIRFFPQALNPAFKDXYKQLPLGAGVDRKQFMRYFAGNLASG	120
Oy	121	GAAGATSLCFEYVPLDFAFRTLADVGRR-AOREFHGLJGDCIIKFKSDGLGLYOGFNVS	179
Db	121	GAAGATSLCFEYVPLDFAFRTLADVAGAGAEERFERGJGDCIYKFKSDGIKGLYOGFNVS	180
Oy	180	VQGIITIRAAAFGYVDPAKGLPDPKKNVHIVFSNMIAQSVTAAVAGLLSPEDTVRRRMM	239
Db	181	VQGIITIRAAAFGYIDPAKGLPDPKKNVHIIYSMIMQYTAAVAGLLSPEDTVRRRMM	240
Oy	240	QSGRKGADIMTYGVDCMRKTAKEBGAKAFFKGMASVNLGMSGAFVLYLDELTKY	296
Db	241	QSGRKGADIMTYGLDLCWRKTAKEBGAKAFFKGMASVNLKMSGAFVLYLDELTKY	297

```

RESULT 5
US-09-811-094-33
: Sequence 33, Application US/09811094
: Patent No. US20010044144A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Clevenger, William
: APPLICANT: Willey, Sandra Eileen
: APPLICANT: Willey, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pel, Yazlong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT)
: TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660088,42004
: CURRENT APPLICATION NUMBER: US/09/811,094
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 33
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Homo sapien
: US-09-811-094-33

```

Query Match	89.28;	Score 1385.5;	DB 10;	Length 298;
Best Local Similarly	87.28;	Pred. No. 5.5e-137;		
Matches 260;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 1.

[illegible]

RESULT 6

```

US-09-810-644-33
Sequence 33, Application US/09810644
Patent No. US20020012992A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT FILING DATE: US/09/810, 644
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-810-644-33

Query Match      89.2%; Score 1385.5; DB 10; Length 298;
Best Local Similarity 87.2%; Pred. No. 5.5e-137;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 14

```

Oy		1	MGHANSTLKEPFLAGAVAAANASTPAVAPIEBVKLLLOVOHAKSOISAEKQYKGIIDCVR	60
Dd		1	MTBOAISAKPFLGAGLIAIAKSTPAVAIEBVKLLLOVOHAKSOIADAKOIKGIVD.IVR	60
Oy		61	IPKEGGLSEWRGNLANVIREFPTQALNFAEKDKYKOLPLGVDRHKOFMRYPAGNLASG	120
Dd		61	IPKEGVLSFWRGNLANVIREFPTQALNFAEKDKYKOIPLGVDRKHQFMRYPAGNLASG	120
Oy		121	GAAGTSLCFEYUPLDPATRLAABVGRR-AOREPHGIGDCILIKFKESDGJRGLYOGPNVS	179
Dd		121	GAAGTSLCFEYUPLDPATRLAABVGSGTEREBERGGDDCLVKTYSKDSJRGLYOGSVS	180
Oy		180	VQGIIIFYBAAYFGVYDTAKGMLDPBKVNHTFVSNMIAOSQSYTAAVAGLLSPEDFYRRMM	239
Dd		181	VQGIITYBAAYFGVYDTAKGMLDPBKNTHTIVSNMIAOQTAAVAGVSYEPDFYRRMM	240
Oy		240	OSGRKGADIMTYGVDCNRKTAKEDEGAKAFFPKGMSNVLAGMGCAFVLVLYDELKTV	297
Dd		241	OSGRKGADIMTYGVDCNRKTFREDEGGAFAPFKGMSNVLRMGCAFVLVLYDELKTV	298

```

? RESULT 7
? US-09-801-368-252
? Sequence 252, Application US/09801368
? Patent No. US20020128250A1
? GENERAL INFORMATION:
? APPLICANT: Busby, Robert
? APPLICANT: Cali, Brian
? APPLICANT: Hecht, Peter
? APPLICANT: Holtzman, Doug
? APPLICANT: Madden, Kevin
? APPLICANT: Maxon, Mary
? APPLICANT: Milne, Todd
? APPLICANT: No. US20020128250A1man, Thea
? APPLICANT: Royer, John
? APPLICANT: Salama, Sofie
? APPLICANT: Sherman, Amir
? APPLICANT: Silva, Jeff
? APPLICANT: Summers, Eric
? TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
? FILE REFERENCE: 109272.147
? CURRENT APPLICATION NUMBER: US/09/801,368
? CURRENT FILING DATE: 2001-03-07

```

;; PRIOR APPLICATION NUMBER: US 09/487,558
;; PRIOR FILING DATE: 2000-01-19
;; PRIOR APPLICATION NUMBER: US 60/160,587
;; PRIOR FILING DATE: 1999-10-20
;; NUMBER OF SEQ ID NOS: 440
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 252
;; LENGTH: 318
;; TYPE: PRF
;; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-252

Query Match 47.3%; Score 734; DB 10; Length 318;
Best Local Similarity 53.2%; Pred. No. 4.9e-69;

Matches 156; Conservative 45; Mismatches 82; Indels 10; Gaps 5;

QY 7 SFLKDLFAGVAAVASTAAPTIERVKLLQOV-HASKQISAERQYGIIDCVRIPEKQ 65
DB 22 NPLIDFLMGVSAVASTAAPTIERVKLLQONDEMLKSGRLSHPKGIGECPSRTVKDE 81
QY 66 GFLSPWGNLANVIRYPTQALNFAFKDKYKOLFLGVDNRHKOFRYFAGNLASGAGA 125
DB 82 GVTSFMRGNANVIRYPTQALNFAFKDKIKAMF-GFKKEGAKMFAENLASGAGA 139
QY 126 TSLCFVYPLDFARTRLAAD--VGRRAQREPHGLDCTIIFKSDGLRGLYOGFNVSOG 182
DB 140 LSLFLVYSLDYARTRLAADSSKKGAROFNGLIDYKKTLSGVAAGLGRFLPSVVG 159
QY 183 IITIRAAVFGVYDPAKMLDPKVNHFV--SMIAQSVTAAGLISVPTVRRMMOS 241
DB 200 IIVYRGILFMYDSLAKLLTGLSEGSFLASFLGAVVYTGASTCSTPDLTVRRMMTS 259
QY 242 GRKGADIMYGTGVCWRIKADGAKAFKGAWSNVLRGAGFVLVYDEIK 294
DB 260 GQA---VKYDGAEDCLKRIYAEGVSGSLFKGCAGNLLRGVAGVISMVQLQ 309

RESULT 8
US-09-734-569-170

;; Sequence 170, Application US/09734569
;; Patent No. US20020064816A1

;; GENERAL INFORMATION:

;; APPLICANT: Lerchl, Jens
;; APPLICANT: Renz, Andreas
;; APPLICANT: Ehrhardt, Thomas
;; APPLICANT: Reinold, Andreas
;; APPLICANT: Cirpus, Petra
;; APPLICANT: Bischoff, Friedrich
;; APPLICANT: Frank, Markus
;; APPLICANT: Freund, Annette
;; APPLICANT: Duwenig, Elke
;; APPLICANT: Schmidt, Ralf-Michael
;; APPLICANT: Reski, Ralf
;; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
;; FILE REFERENCE: In the synthesis of carbohydrates
;; CURRENT APPLICATION NUMBER: US/09/734,569
;; CURRENT FILING DATE: 2001-05-24
;; PRIOR APPLICATION NUMBER: US 60/171,101
;; PRIOR FILING DATE: 1999-12-16
;; NUMBER OF SEQ ID NOS: 181
;; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
;; SEQ ID NO 170
;; LENGTH: 386
;; TYPE: PRF
;; ORGANISM: Physcomitrella patens
US-09-734-569-170

Query Match 47.3%; Score 734; DB 10; Length 386;
Best Local Similarity 52.9%; Pred. No. 6.2e-69;
Matches 156; Conservative 43; Mismatches 84; Indels 12; Gaps 6;

QY 7 SFLKDLFAGVAAVASTAAPTIERVKLLQOV-HASKQISAERQYGIIDCVRIPEKQ 65

DB 84 SFMTDFLMGVSAVASTAAPTIERVKLLQONDEMLKSGRLSHPKGIGECPSRTVKDE 143
QY 66 GFLSPWGNLANVIRYPTQALNFAFKDKYKOLFLGVDNRHKO-FWRYFAGNLASGAGA 124
DB 144 GMSLWGNLANVIRYPTQALNFAFKDKYKSLF--GYKKDKGYKMFAGNLASGAGA 201
QY 125 ATSLCFVYPLDFARTRLAADVGR--AOREPHGLDCTIIFKSDGLRGLYOGFNVS 180
DB 202 ASSLLFVYSLDYARTRLAADSSKKGAROFNGLIDYKKTLSGVAAGLGRFLPSVVG 261
QY 181 OGITIRAAVFGVYDPAK-MLPDPKVNHFVSMIAQSVTAAGLISVPTVRRMM 239
DB 262 AGIIVYRGILFMYDSLAKLLTGLSEGSFLASFLGAVVYTGASTCSTPDLTVRRMM 321
QY 240 QSRKGADIMYGTGVCWRIKADGAKAFKGAWSNVLRGAGFVLVYDEIK 294
DB 322 TSGBA---VKYNGMDAFKQILAKEGAKSLFKGAGNLLRGVAGVISMVQLQ 373

RESULT 9
US-09-925-301-1459

;; Sequence 1459, Application US/09925301

;; Patent No. US20020052308A1

;; GENERAL INFORMATION:

;; APPLICANT: Rosen et al.

;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

;; FILE REFERENCE: PA106

;; CURRENT APPLICATION NUMBER: US/09/925,301

;; CURRENT FILING DATE: 2001-08-10

;; PRIOR APPLICATION NUMBER: PCT/US00/05892

;; PRIOR FILING DATE: 2000-03-08

;; PRIOR APPLICATION NUMBER: 60/124,270

;; PRIOR FILING DATE: 1999-03-12

;; NUMBER OF SEQ ID NOS: 1694

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 1459

;; LENGTH: 132

;; TYPE: PRF

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: SITE

;; LOCATION: (115)

;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

;; NAME/KEY: SITE

;; LOCATION: (123)

;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

;; NAME/KEY: SITE

;; LOCATION: (126)

;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

;; NAME/KEY: SITE

;; LOCATION: (129)

;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-301-1459

Query Match 29.7%; Score 461; DB 10; Length 132;
Best Local Similarity 83.0%; Pred. No. 4.6e-41;

Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MGDHWSFLKDLFAGVAAVASTAAPTIERVKLLQOVHASKQISAERQYGIIDCVRI 60
DB 26 MTEQALSFARDFLAGGIAAISTAVAPIERVKLLQOVHASKQIADKQKIVDCIVR 85
QY 61 IPKEQGLSPWGNLANVIRYPTQALNFAFKDKYKOLFLGVDNRH 106
DB 86 IPKEQGLSPWGNLANVIRYPTQALNFAFKDKYKQXFLGXVXKH 131

RESULT 10
US-09-864-761-36440
;; Sequence 36440, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:

```

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 36440
LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO L7810.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALU6 6.00e-38
OTHER INFORMATION: EST_HUMAN HIT: AW935235.1, EVALU6 5.00e-37
US-09-864-761-36440

```

[illegible]

```

Db          1  FAGNIASGGAAGANTSLCFVPLDFARTRLADVGKAGEREFGIDCLVIKXSDGIK 60
OY          172  LYGFNFNSVGGIIITYRAAYFGVYDTAK 198
             |||||
Db          61  LYGFNFNSVGGIIITYRAAYFGVYDTAK 87
             |||||

RESULT 11
US-09-777-921A-4
; Sequence 4, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
; FILE REFERENCE: C0001103
; CURRENT APPLICATION NUMBER: US/09/777, 921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-777-921A-4

```

	Query Match	22.6%	Score 350.5	DB 10	Length 475
	Best Local Similarity	32.3%	Pred. No. 7.7e-29		
	Matches 95	Conservative 55	Mismatches 115	Indels 29	Gaps 9
Qy	10	KDPLAGAAVAAANSKRAVAVPIERVKLLTLLVOHAKSDIAAEKOVKGIIDCVRIPIKEOGFLS	69		
Db	196	ROLLAGGAGAAASRSTSTPLDLRLKAMVOY-HGSKSMNIFGGRQMI-----KKGGRS	247		
Qy	70	FWRGAGVAVIRYFYPQALNFAFKDKYKQIFLEGVDRHKKQFWRYFAGNLAGSAGAAATSLC	129		
Db	248	LMRGKGTAVIKAPIETAFAKFWYEDYKRLPIKEGOKIGTFEERFISGM-----ACATATQ	302		
Qy	130	FVYPLDFAFRTLAAVDVGRRAREFHGLGDCIIKIFKSDGLRGLYOGFVNVYOGIITRYAA	189		
Db	303	FLYPEWVKMTRLA--VGKTRQ--YSGIYDCAKKILKIEGAFYKGYVPLNLGIIPYAGI	358		
Qy	190	YFGVVDIAK-----GMLDPKKNVHLFVSMIAQSTAAVAGLSITPEPDYVRRPMAMOSGRK	244		
Db	359	DLAVVELKSHWLDFNFAQDSVNPQVLVYLIGCGALSTSCGQLASYPALATVRTMQAOAMDE	418		
Qy	245	GADIVYTGTVQDCWKRIADDEGAKAFPKGAMSN---VLKRMGAFPLVLYDELTK	295		
Db	419	GAPOL--MMVGLFRRIRIKESGILPGLIRGTTPMFKMLPAPVGSISY--VYVENKKO	468		

```

RESULT 12
US-09-777-921A-2
: Sequence 2, Application US/09777921A
: Patent No. US20020115136A1
: GENERAL INFORMATION:
: APPLICANT: MERKULOV et al.
: TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CL001103
: CURRENT APPLICATION NUMBER: US/09/777,921A
: CURRENT FILING DATE: 2002-02-07
: NUMBER OF SEQ. ID NOS: 126
: SOFTWARE: PasteSeq for Windows Version 4.0
: SEQ. ID NO. 2
: LENGTH: 477
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-777-921A-2

```

Query Match	22.3%	Score 346.5	DB 10	Length 477
-------------	-------	-------------	-------	------------

[illegible]

```

RESULT 13
US-09-777-921A-5
: Sequence 5, Application US/09777921A
: Patent No. US20020115136A1
: GENERAL INFORMATION:
: APPLICANT: MERKULOV et al.
: TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CL001103
: CURRENT APPLICATION NUMBER: US/09/777,921A
: CURRENT FILING DATE: 2002-02-07
: NUMBER OF SEQ ID NOS: 126
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 410
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-777-921A-5

```

Query Match	20.1%	Score 312	DB 10	Length 410
Best Local Similarity	34.6%	Pred. No. 6.6e-25		
Matches 82; Conservative	41	Mismatches 94	Indels 20	Gaps 7

[illegible]

RESULT 14
US-09-992-598-289
: Sequence 289, Application US/09992598
: Patent No. US20020160384A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David

1 APPLICANT: Desnoyers, Luc
2 APPLICANT: Eaton, Dan L.
3 APPLICANT: Ferrara, Napoleone
4 APPLICANT: Fong, Sherman
5 APPLICANT: Gerber, Hanspeter
6 APPLICANT: Gerritsen, Mary E.
7 APPLICANT: Goddard, Audrey
8 APPLICANT: Godowski, Paul J.
9 APPLICANT: Grimaldi, J. Christopher
10 APPLICANT: Gurney, Austin L.
11 APPLICANT: Klyavin, Ivar J.
12 APPLICANT: Napier, Mary A.
13 APPLICANT: Pan, James
14 APPLICANT: Paoni, Nicholas F.
15 APPLICANT: Roy, Margaret Ann
16 APPLICANT: Stewart, Timothy A.
17 APPLICANT: Tumas, Daniel
18 APPLICANT: Watanabe, Colin K.
19 APPLICANT: Williams, P. Mickey
20 APPLICANT: Wood, William I.
21 APPLICANT: Zhang, Zemin
22
23 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
24
25 FILE REFERENCE: P2730PIC20
26
27 CURRENT APPLICATION NUMBER: US/09/992,598
28
29 CURRENT FILING DATE: 2001-11-14
30
31 PRIOR APPLICATION NUMBER: 60/049787
32
33 PRIOR FILING DATE: 1997-06-16
34
35 PRIOR APPLICATION NUMBER: 60/062250
36
37 PRIOR FILING DATE: 1997-10-17
38
39 PRIOR APPLICATION NUMBER: 60/065186
40
41 PRIOR FILING DATE: 1997-11-12
42
43 PRIOR APPLICATION NUMBER: 60/065311
44
45 PRIOR FILING DATE: 1997-11-13
46
47 PRIOR APPLICATION NUMBER: 60/066770
48
49 PRIOR FILING DATE: 1997-11-24
50
51 PRIOR APPLICATION NUMBER: 60/075945
52
53 PRIOR FILING DATE: 1998-02-25
54
55 PRIOR APPLICATION NUMBER: 60/078910
56
57 PRIOR FILING DATE: 1998-03-20
58
59 PRIOR APPLICATION NUMBER: 60/083322
60
61 PRIOR FILING DATE: 1998-04-28
62
63 PRIOR APPLICATION NUMBER: 60/084600
64
65 PRIOR FILING DATE: 1998-05-07
66
67 PRIOR APPLICATION NUMBER: 60/087106
68
69 PRIOR FILING DATE: 1998-05-28
70
71 PRIOR APPLICATION NUMBER: 60/087607
72
73 PRIOR FILING DATE: 1998-06-02
74
75 PRIOR APPLICATION NUMBER: 60/087609
76
77 PRIOR FILING DATE: 1998-06-02
78
79 PRIOR APPLICATION NUMBER: 60/087759
80
81 PRIOR FILING DATE: 1998-06-02
82
83 PRIOR APPLICATION NUMBER: 60/087827
84
85 PRIOR FILING DATE: 1998-06-03
86
87 PRIOR APPLICATION NUMBER: 60/088021
88
89 PRIOR FILING DATE: 1998-06-04
90
91 PRIOR APPLICATION NUMBER: 60/088025
92
93 PRIOR FILING DATE: 1998-06-04
94
95 PRIOR APPLICATION NUMBER: 60/088026
96
97 PRIOR FILING DATE: 1998-06-04
98
99 PRIOR APPLICATION NUMBER: 60/088028
100
101 PRIOR FILING DATE: 1998-06-04
102
103 PRIOR APPLICATION NUMBER: 60/088029
104
105 PRIOR FILING DATE: 1998-06-04
106
107 PRIOR APPLICATION NUMBER: 60/088030
108
109 PRIOR FILING DATE: 1998-06-04
110
111 PRIOR APPLICATION NUMBER: 60/088033
112
113 PRIOR FILING DATE: 1998-06-04
114
115 PRIOR APPLICATION NUMBER: 60/088326
116
117 PRIOR FILING DATE: 1998-06-04
118
119 PRIOR APPLICATION NUMBER: 60/088167
120
121 PRIOR FILING DATE: 1998-06-05
122
123 PRIOR APPLICATION NUMBER: 60/088202
124

```

1  PRIOR APPLICATION NUMBER: 60/090444
2  PRIOR FILING DATE: 1998-06-24
3  PRIOR APPLICATION NUMBER: 60/090445
4  PRIOR FILING DATE: 1998-06-24
5  PRIOR APPLICATION NUMBER: 60/090472
6  PRIOR FILING DATE: 1998-06-24
7  PRIOR APPLICATION NUMBER: 60/090535
8  PRIOR FILING DATE: 1998-06-24
9  PRIOR APPLICATION NUMBER: 60/090540
10 PRIOR FILING DATE: 1998-06-24
11 PRIOR APPLICATION NUMBER: 60/090542
12 PRIOR FILING DATE: 1998-06-24
13 PRIOR APPLICATION NUMBER: 60/090557
14 PRIOR FILING DATE: 1998-06-24
15 PRIOR APPLICATION NUMBER: 60/090676
16 PRIOR FILING DATE: 1998-06-25
17 PRIOR APPLICATION NUMBER: 60/090678
18 PRIOR FILING DATE: 1998-06-25
19 PRIOR APPLICATION NUMBER: 60/090690
20 PRIOR FILING DATE: 1998-06-25
21 PRIOR APPLICATION NUMBER: 60/090694
22 PRIOR FILING DATE: 1998-06-25
23 PRIOR APPLICATION NUMBER: 60/090695
24 PRIOR FILING DATE: 1998-06-25
25 PRIOR APPLICATION NUMBER: 60/090696
26 PRIOR FILING DATE: 1998-06-25
27 PRIOR APPLICATION NUMBER: 60/090862
28 PRIOR FILING DATE: 1998-06-26
29 PRIOR APPLICATION NUMBER: 60/090863
30 PRIOR FILING DATE: 1998-06-26
31 PRIOR APPLICATION NUMBER: 60/091360
32 PRIOR FILING DATE: 1998-07-01
33 PRIOR APPLICATION NUMBER: 60/091478
34 PRIOR FILING DATE: 1998-07-02
35 PRIOR APPLICATION NUMBER: 60/091544
36 PRIOR FILING DATE: 1998-07-01
37 PRIOR APPLICATION NUMBER: 60/091519
38 PRIOR FILING DATE: 1998-07-02
39 PRIOR APPLICATION NUMBER: 60/091626
40 PRIOR FILING DATE: 1998-07-02
41 PRIOR APPLICATION NUMBER: 60/091633
42 PRIOR FILING DATE: 1998-07-02
43 PRIOR APPLICATION NUMBER: 60/091978
44 PRIOR FILING DATE: 1998-07-07
45 PRIOR APPLICATION NUMBER: 60/091982
46 PRIOR FILING DATE: 1998-07-07
47 PRIOR APPLICATION NUMBER: 60/092182
48 PRIOR FILING DATE: 1998-07-09
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856

```

OY 292 EIR 294
: 1
Db 459 NLK 461

RESULT 15
US-09-989-722-289
: Sequence 289, Application US/09989722
: Patent No. US20020072067A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botslein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerltisen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730PLC63
: CURRENT APPLICATION NUMBER: US/09/989,722
: PRIOR FILING DATE: 2001-11-19
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
: PRIOR APPLICATION NUMBER: 60/087607
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087609
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087759
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087827
: PRIOR FILING DATE: 1998-06-03
: PRIOR APPLICATION NUMBER: 60/088021
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088025
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088026
: PRIOR FILING DATE: 1998-06-04

: PRIOR APPLICATION NUMBER: 60/088028
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088029
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088030
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088033
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088326
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088167
: PRIOR FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 60/088202
: PRIOR FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 60/088212
: PRIOR FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 60/088217
: PRIOR FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 60/088655
: PRIOR FILING DATE: 1998-06-09
: PRIOR APPLICATION NUMBER: 60/088734
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088738
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088742
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088810
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088824
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088826
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088858
: PRIOR FILING DATE: 1998-06-11
: PRIOR APPLICATION NUMBER: 60/088861
: PRIOR FILING DATE: 1998-06-11
: PRIOR APPLICATION NUMBER: 60/088876
: PRIOR FILING DATE: 1998-06-11
: PRIOR APPLICATION NUMBER: 60/089105
: PRIOR FILING DATE: 1998-06-12
: PRIOR APPLICATION NUMBER: 60/089440
: PRIOR FILING DATE: 1998-06-16
: PRIOR APPLICATION NUMBER: 60/089512
: PRIOR FILING DATE: 1998-06-16
: PRIOR APPLICATION NUMBER: 60/089514
: PRIOR FILING DATE: 1998-06-16
: PRIOR APPLICATION NUMBER: 60/089532
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089538
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089598
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089599
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089600
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089653
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089801
: PRIOR FILING DATE: 1998-06-18
: PRIOR APPLICATION NUMBER: 60/089907
: PRIOR FILING DATE: 1998-06-18
: PRIOR APPLICATION NUMBER: 60/089908
: PRIOR FILING DATE: 1998-06-18
: PRIOR APPLICATION NUMBER: 60/089947
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: 60/089948
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: 60/089952
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: 60/090246
: PRIOR FILING DATE: 1998-06-22
: PRIOR APPLICATION NUMBER: 60/090252

```

; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
;
Query Match      19.6%; Score 304; DB 10; Length 469;
Best Local Similarity 29.0%; Pred. No. 5.3e-24;
Matches 88; Conservative 58; Mismatches 115; Indels 42; Gaps 11;
```

```

QY      6  WSEFKDFLAGAANAASVTAVPERVKLLYOAHASKQISAEKQYGIIDCVIRPKEQ 65
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 187  WRHL-----VAGGAGAVSRTCTAPLDRKLVLMQV-HASR-----SNNMGITGGFTQMTREG 237
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      66  GLISFWNGNLANYIRYFPTQALNFAFKDKYKOLFLGGVDR-----HKQFWRYFAGNLASG 120
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 238  GARSLWNGNGINVLKIPESAIKFMAYEQIKRLV--GSDQETLRIHER-----LVAG 287
```

```

QY      121  GAAGATSLCFVYPLDPAFTRPLADVGRRARPERHGLDCTIKIFKSDGLNGLYQGENVSV 180
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 288  SLGATAAOSSTIYPMEEVLKTFMAL-----RKTGOYSGMLDCARRILAREGVAAPFKGYVPM 343
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      181  OGIIYRAAFGYVDPAKGM-----LPDPKNVHIFVSWMTAQSVAAGLSYPDFT 232
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 344  LGIIPYAGIDLAAYETLKNMLOHYAVNSADP---GVFVLLACGTMSSTGQLASTPLAL 400
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      233  VRRRMWQSGRGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFV-LVLYD 291
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 401  VPRMQAQASTEGAPEVTMSSL--FKHILRTEGAFGLRGLADNPMKVIIPAVSISYVYE 458
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY      292  EIK 294
      |  |
DB      459  NLK 461
```

Search completed: November 12, 2002, 16:56:55
Job time : 7.31915 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:05 ; Search time 13.9686 Seconds

(without alignments)
2044.001 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGVA...LRMGCAFVLYLDEIKKV 297Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526.5	98.3	298	1 A44778	ADP/ATP carrier pr
2	1463.5	94.4	298	2 I60173	adenine nucleotide
3	1463.5	94.2	298	1 S37210	ADP/ATP carrier pr
4	1458.5	93.9	298	1 XWBO	ADP/ATP carrier pr
5	1391.5	89.6	298	1 A29132	ADP/ATP carrier pr
6	1385.5	89.2	298	1 S03894	ADP/ATP carrier pr
7	1380.5	88.9	298	2 B43646	ADP/ATP carrier pr
8	1368.5	88.1	298	2 S31814	ADP/ATP carrier pr
9	1142.5	67.3	301	1 S31935	ADP/ATP carrier pr
10	1045.5	67.3	313	2 T25850	hypothetical prote
11	1043.5	67.2	313	2 T23207	hypothetical prote
12	1037.5	66.8	300	2 T25371	hypothetical prote
13	1005.5	64.7	300	2 T15206	hypothetical prote
14	973.5	62.7	339	2 A41677	ADP/ATP carrier pr
15	904.5	58.2	301	2 S51132	ADP/ATP carrier pr
16	772	49.7	306	2 T20012	hypothetical prote
17	770.5	49.6	308	1 S30259	ADP/ATP carrier pr
18	756.5	48.7	387	2 S14876	ADP/ATP carrier pr
19	752.5	48.5	322	2 T40526	ADP/ATP carrier pr
20	752.5	48.5	386	2 T09709	ADP/ATP carrier pr
21	751.5	48.4	387	2 S16568	ADP/ATP carrier pr
22	746.5	48.1	379	2 T04608	ADP/ATP carrier pr
23	746.5	48.1	382	2 S33630	ADP/ATP carrier pr
24	745.5	48.0	326	2 T25728	hypothetical prote
25	745.5	48.0	386	2 S17917	ADP/ATP carrier pr
26	744.5	47.9	386	2 S21974	ADP/ATP carrier pr
27	740	47.6	379	2 S21313	ADP/ATP carrier pr
28	740	47.6	386	2 S14874	ADP/ATP carrier pr
29	737	47.5	385	1 S29852	ADP/ATP carrier pr

30	736	47.4	307	2 A36582	ADP/ATP carrier pr
31	734	47.3	318	1 A31978	ADP/ATP carrier pr
32	733.5	47.2	313	1 XWNC	ADP/ATP carrier pr
33	729	46.9	305	2 S68154	ADP/ATP carrier pr
34	728.5	46.9	306	2 T42011	ADP/ATP carrier pr
35	718.5	46.3	309	2 A24849	ADP/ATP carrier pr
36	676	43.5	298	2 T24029	hypothetical prote
37	508	32.7	327	2 T51577	ADP/ATP translocas
38	368	23.7	415	2 T48171	hypothetical prote
39	367.5	23.7	325	2 T04273	hypothetical prote
40	363	23.4	381	2 T51158	hypothetical prote
41	350.5	22.6	475	2 T50686	peroxisomal Ca-dep
42	349.5	22.5	352	2 T01729	mitochondrial solu
43	345.5	22.2	358	2 T45934	hypothetical prote
44	334.5	21.5	348	2 D84798	probable mitochond
45	327	21.1	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1
A44778
ADP/ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP/ATP translocase 1
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence, revision 17-Mar-2000 #text, change 17-Mar-2000
C:Accession: A44778; S03893; A39891; A28116
R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, J. Biol. Chem. 264, 13998-14004, 1989
A>Title: A human muscle adenine nucleotide translocator gene has four exons, its local
A:Reference number: A44778; MVID:89340499; PMID:2547778
A:Accession: A44778
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LIA>
A:Cross-references: GB:J04982; NID:q178658; PIDN:AAA51736.1; PID:q178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATF
A:Reference number: S03893; MVID:89236396; PMID:2541251
A:Accession: S03893
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A>Title: CDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a lea
A:Reference number: A39891; MVID:88041149; PMID:2823266
A:Accession: A39891
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 'A', '17-146, 'RR', '149, '151-226, 'U', '228-298 <NEC>
A:Cross-references: GB:J02966; NID:q339919; PIDN:AAA61223.1; PID:q339920
R:Houlsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level i
A:Reference number: A94197; MVID:88124845; PMID:2829183
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOU>
A:Cross-references: GB:J03593; NID:q339724; PIDN:AAA36751.1; PID:q339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANTL1, T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; Transmembrane protein
F:2-298/Product: ADP/ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACCP3>

Query Match	98.3%;	Score 1526.5;	DB 1;	Length 298;
Best Local Similarity	98.3%;	Pred. No. 1.6e-130;		
Matches 293; Conservative	2;	Mismatches 2;	Indels 1;	Gaps 1;

Qy	1	MGDHA	MS	LK	QF	FL	GA	VAAA	SK	TA	VA	IE	EV	KL	LLO	Y	HA	SK	IO	SA	EK	YK	GI	II	DC	VR	60																														
Db	1	MGDHA	MS	LK	QF	FL	GA	VAAA	SK	TA	VA	IE	EV	KL	LLO	Y	HA	SK	IO	SA	EK	YK	GI	II	DC	VR	60																														
Qy	61	IP	KE	GE	LS	FW	R	G	L	A	N	I	R	E	P	T	O	A	L	F	A	R	K	D	Y	K	O	L	E	G	S	V	D	R	H	K	O	F	W	Y	F	A	G	N	L	A	S	G	120								
Db	61	IP	KE	GE	LS	FW	R	G	L	A	N	I	R	E	P	T	O	A	L	F	A	R	K	D	Y	K	O	L	E	G	S	V	D	R	H	K	O	F	W	Y	F	A	G	N	L	A	S	G	120								
Qy	121	GA	AG	T	S	L	C	F	E	Y	P	L	D	E	F	A	T	R	I	L	A	D	V	G	R	-	R	A	O	R	E	F	H	G	L	D	C	I	I	K	I	P	K	S	O	G	L	E	G	L	O	G	F	N	V	S	170
Db	121	GA	AG	T	S	L	C	F	E	Y	P	L	D	E	F	A	T	R	I	L	A	D	V	G	R	-	R	A	O	R	E	F	H	G	L	D	C	I	I	K	I	P	K	S	O	G	L	E	G	L	O	G	F	N	V	S	180
Qy	180	V	O	G	I	I	T	R	A	A	F	E	G	V	D	T	A	K	G	M	L	P	E	K	N	A	N	H	I	E	V	S	N	M	I	A	O	S	T	A	V	A	G	L	S	P	E	D	T	V	R	R	R	M	230		
Db	181	V	O	G	I	I	T	R	A	A	F	E	G	V	D	T	A	K	G	M	L	P	E	K	N	A	N	H	I	E	V	S	N	M	I	A	O	S	T	A	V	A	G	L	S	P	E	D	T	V	R	R	R	M	240		
Qy	240	Q	S	G	R	G	A	I	M	T	G	V	D	C	A	R	K	T	A	K	D	E	G	A	A	F	E	K	G	A	S	N	L	R	B	M	G	A	F	Y	L	V	L	D	E	I	K	K	Y	297							
Db	241	Q	S	G	R	G	A	I	M	T	G	V	D	C	A	R	K	T	A	K	D	E	G	A	A	F	E	K	G	A	S	N	L	R	B	M	G	A	F	Y	L	V	L	D	E	I	K	K	Y	298							

RESULT 2

adenine nucleotide translocator - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: I60173
R:Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
B:Biochem. Biophys. Acta 1152, 192-196, 1993
A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat
A:Reference number: I60173; MUID:94002161; PMID:8399300
A:Accession: I60173
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1*298 <RES>
A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
A:Genetics:
A:Gene: antl
A:Introns: 37/3; 200/1; 247/1
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACR1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACR2>
F:207-238/Domain: ADP,ATP carrier protein repeat homology <ACR3>

Query Match	94.4%	Score 1466.5	DB 2	Length 298
Best Local Similarity	94.3%	Pred. No. 4.3e-125		
Matches	281	Conservative	9	Mismatches 7; Indels 1; Gaps 1;
QY	1	MGDHAMSELDKFLAGAAVAANAKTAVAEIERVKLLLYQHASKQISAQKQYKGIIDCYVR	60	
Db	1	MGDQLSTELDKPDLAGGIAAASKTAVADIERVKLLLYQHASKQISAQKQYKGIIDCYVR	60	
QY	61	IPKEGFLSPFRGNLANIYIRPTQALNFAEKDKKQLFLGVDNHHKQFWRIFAGNLASG	120	
Db	61	IPKEGFLSPFRGNLANIYIRPTQALNFAEKDKKQIFLGVDNHHKQFWRIFAGNLASG	120	
QY	121	GAAGATSLCFVYPLDPFARTLADAYGR-RAOREFGLGICCIIRKPSGRLYOGFPWS	179	
Db	121	GAAGATSLCFVYPLDPFARTLADAYGRSSQREFNGLDCLIRKPSGRLYOGFPWS	180	
QY	180	VQGIITIRAAAYFGVYDTAKGMLPDEKNHIIFYSMWIAQSVTAAGLLSPEDTVRRMM	239	
Db	181	VQGIITIRAAAYFGVYDTAKGMLPDEKNHIIYSMWIAQSVTAAGLLSPEDTVRRMM	240	
QY	240	QSGRGALIMTGTCTDCMRKIAKDGCAAFKFGANSNVLRGMGAFVLYLDEIKKY	297	

Db 241 QSGRKGADIMYTGTVDCWRKIAKDEGRKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 3

ADP,ATP carrier protein T1 - mouse
 N:Alternate names: adenine nucleotide carrier
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S37210
 R:Laplace, C.; Costet, P.
 submitted to the EMBL Data Library, September 1993
 A:Reference number: S37210
 A:Accession: S37210
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <LAP>
 A:Cross-references: EMBL:X74510; NID:g402627; PIDN:CAAS2616.1; PID:g402628
 C:Genetics:
 A:Gene: ANCI
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication, transmembrane protein
 F:5-39/Domains: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domains: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-238/Domains: ADP,ATP carrier protein repeat homology <ACP3>

Query Match	94.2%;	Score 1463.5;	DB 2;	Length 298;
Best Local Similarity	94.0%;	Pred. No. 8e-125;		
Matches 280;	Conservative 10;	Mismatches 7;	Indels 1;	Gaps 1;

QY	1	MGAMSLKDFLAGNAAAVSTPAAPERVYLLLOVOHASKOISAEKQYGIIDCVR	60
QY	1	MGDMSTLSTKDFLAGGIAAAVSTPAAPERVALLLOVOHASKOISAEKQYGIIDCVR	60
QY	61	IPKEDGFLSEWRGNLANVIRPPTQALNFAEKDKYKQELGVDYRHQKQWRYFAQNLASG	120
QY	61	IPKEGFLSEWRGNLANVIRPPTQALNFAEKDKYKQELGVDYRHQKQWRYFAQNLASG	120
QY	121	GAACTSLCFYPLDFAFRTPLADYVG-RAQREPHLGICCIKIPKSOBLTGQFVNS	179
QY	121	GAACTSLCFYPLDFAFRTPLADYVGSSQREPNGLDCLTRFNSDGLKCLYGFESVS	180
QY	180	VQGIITRYAAAFYGVYDPAKAGMLDPKKNVHIFYSWMLAQSVYAVAGLSYFPDFTVRMM	239
QY	181	VQGIITRYAAAFYGVYDPAKAGMLDPKKNVHIFYSWMLAQSVYAVAGLSYFPDFTVRMM	240
QY	240	QSGRGKADIMTGTVDWCRRKIADDEGAKAFKFKANSNVLRKMGAGVLYLYDEIKKY	297
QY	241	QSGRGKADIMTGTGLDWCRRKIADDEGANAFFKAKANSNVLRKMGAGVLYLYDEIKKY	298

RESULT 4

ADP,ATP carrier/protein T1 - bovine
N:Alternate names: ADP/ATP translocase T1
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
C:Accession: A43646; A24922; A03181; A61343; S63369
R:Powell, S.J.; Mead, S.M.; Runswick, M.J.; Walker, J.F.
Biochemistry 28, 866-873, 1989
A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently
A:Reference number: A43646; MUID:89223093; PMID:2540808
A:Accession: A43646
A:Molecule type: mRNA
A:Residues: 1-298 <Pov>
A:Cross-references: GS:M4102; NID:g529414; PIDN:AAA30768.1; PID:g529415
R:Basmussen, U.B.; Mohlirab, H.
Biochem Biophys. Res. Commun. 138, 850-857, 1986
A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unus
A:Reference number: A24822; MUID:86295775; PMID:3017341
A:Accession: A24822
A:Molecule type: mRNA
A:Residues: 208-298<RAS>

A:Gene: GDB:ANT3; ANT3Y
 A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
 A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:2-298/Product: ADP,ATP carrier protein #status predicted <AMT>
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 89.2%; Score 1385.5; DB 1; Length 298;
 Best Local Similarity 87.2%; Pred. No. 9.1e-118;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 Db 1 MTEQALISPAKDFLAGIAAISKTAVAPIERVKLLQVHASKOIAADKQYKGIIDCVR 60
 QY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 Db 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGR-AQREHGLDCLIKIFKSGDLGLYQGFNVS 179
 Db 121 GAAGATSLCFYYPIDFARTRLAADVGRSGTEREFGLDCLVKTITKSDIGLIGLYQGFNVS 180
 QY 180 VQGIITVRAAFYGYDPAKGMLPDPKNVHIFVSMIAOSVTAVAGLSYEPDTRRRMM 239
 Db 181 VQGIITVRAAFYGYDPAKGMLPDPKNVHIFVSMIAOSVTAVAGVSYEPDTRRRMM 240
 QY 240 QSGRRGADIMYTGTVDCWRKTADEGAKAFKGAWSNVLKMGAFVLYLDELTKKY 297
 Db 241 QSGRRGADIMYTGTVDCWRKIFRDEGKAFKGAWSNVLKMGAFVLYLDELTKKY 298

RESULT 7

ADP,ATP carrier protein T2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: B43646
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.9%; Score 1380.5; DB 2; Length 298;
 Best Local Similarity 86.9%; Pred. No. 2.6e-117;
 Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 Db 1 MTEQALISPAKDFLAGIAAISKTAVAPIERVKLLQVHASKOIAADKQYKGIIDCVR 60
 QY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 Db 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGR-AQREHGLDCLIKIFKSGDLGLYQGFNVS 179
 Db 121 GAAGATSLCFYYPIDFARTRLAADVGRSGTEREFGLDCLVKTITKSDIGLIGLYQGFNVS 180

QY 180 VQGIITVRAAFYGYDPAKGMLPDPKNVHIFVSMIAOSVTAVAGLSYEPDTRRRMM 239
 Db 181 VQGIITVRAAFYGYDPAKGMLPDPKNVHIFVSMIAOSVTAVAGVSYEPDTRRRMM 240
 QY 240 QSGRRGADIMYTGTVDCWRKTADEGAKAFKGAWSNVLKMGAFVLYLDELTKKY 297
 Db 241 QSGRRGADIMYTGTVDCWRKILKDEGKAFKGAWSNVLKMGAFVLYLDELTKKY 298

RESULT 8

ADP,ATP carrier protein T2 - mouse
 N:Alternate names: adenine nucleotide translocase
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
 C:Accession: S31814
 R:Costet, P.; Laplace, C.
 submitted to the EMBL Data Library, January 1993
 A:Reference number: S31814
 A:Accession: S31814
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <COS>
 A:Cross-references: EMBL:X70847
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.1%; Score 1368.5; DB 2; Length 298;
 Best Local Similarity 87.2%; Pred. No. 3.2e-116;
 Matches 259; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 Db 1 MTEQALISPAKDFLAGAANAISKTAVAPIERVKLLQVHASKOIAADKQYKGIIDCVR 60
 QY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 Db 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGR-AQREHGLDCLIKIFKSGDLGLYQGFNVS 179
 Db 121 GAAGATSLCFYYPIDFARTRLAADVGRSGTEREFGLDCLVKTITKSDIGLIGLYQGFNVS 180
 QY 180 VQGIITVRAAFYGYDPAKGMLPDPKNVHIFVSMIAOSVTAVAGLSYEPDTRRRMM 239
 Db 181 VQGIITVRAAFYGYDPAKGMLPDPKNVHIFVSMIAOSVTAVAGLSYEPDTRRRMM 240
 QY 240 QSGRRGADIMYTGTVDCWRKTADEGAKAFKGAWSNVLKMGAFVLYLDELTKKY 296
 Db 241 QSGRRGADIMYTGTVDCWRKTADEGAKAFKGAWSNVLKMGAFVLYLDELTKKY 297

RESULT 9

ADP,ATP carrier protein - African malaria mosquito
 C:Species: Anopheles gambiae (African malaria mosquito)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S31935
 R:Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
 submitted to the EMBL Data Library, February 1993
 A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
 A:Reference number: S31935
 A:Accession: S31935
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-301 <BEA>
 A:Cross-references: EMBL:Z21814; EMBL:Z21815
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;112-204/Domain:	ADP,ATP carrier protein repeat	homology <ACP2>
F;209-300/Domain:	ADP,ATP carrier protein repeat	homology <ACP3>

Query Match	Score	DB 1	Length	301
73.68;	1142.5;			
76.38;	0.14-05			

Matches 221; Conservative 26; Mismatches 42; Indels 1; Gaps 1;

QY 6 WSEFLKQFLAGAAVAAASKTVAIEIVKKLLLYOVHQAOKISAEKQYKGIIDCVNIPREO 65
 :
 Db 8 YGFAXPDLFAGGISAAVSKTAVAIENVKLLLDYQAASAKIANDKOYKGIVDFVNIPREO 67

QY 66 GFLSFMRGNLANIIRIFPTQALNFAPKDKYKOLFTLGVDREHKQMYRFPAGNLASGAAGA 125
 :
 Db 68 GIGAFEGCGNLANIIRYFFPTQALNFAPKDYKOVFLTGVDKNQFYRLFGNLGSSGAGA 127

QY 126 TSLCFEVPPLDFAATRYLAADVGRRA-OREFHGGDCITIKFSDSGLRGLYOGNNVSVOGIT 184
 :
 Db 128 TSLCFEVPPLDFAATRIGADVDYPCGAGERENGLDCLCKTKVKSDDGITLGRGNVSVOGIT 187

QY 185 IYRAAYFGVYDTAKGMLPEPKNVHIIVSNMIAQSOTLVANAGLSYEPEDVVRRRMMQSGRK 244
 :
 Db 188 IYRAAYFGCEDTAKGMLPDKNKTSIFVSMAIQVYTASGIISTYEPDVVRRRMMQNSMPC 247

QY 245 GADIMTYGTVCDRKRTAKDEGAKAFAFKGMAVSNVLKMGCAFVLVLYDEIK 294
 :
 Db 248 KSEVMYKNNTLDGVWKIGKEQGSCAFKGFASVNLRIETGALVLVLYDEVK 297

[illegible][illegible]

Db 68 QGVLSLMRGVNVANVIRYPPQAFNFAPKDYFKNIF-PRYDQNTDESKFECVNIISGATAG 126
QY 125 AFSLCFVYPLDPARTRLADYGRRAQREFFHGLGDCIIEFKSDGLRGLYOGFNNSVQGI 184
Db 127 AISTLIYVPLDPARTRLASDIDGKGRQFTGIFDCLAKIYKOTGLISLXSGFGVSVTGII 186
QY 185 IYRAAYFGVYDTAKGML-PDPKNVHIFVSMIAOSVTAVAGILSYPEPTVRRRMMQSGR 243
Db 187 VYRGSYFGLYDSAKALLFTNDKNTNIVLKMVAQSVTLAAGLISTPEPTVRRRMMMSGR 246
QY 244 KG-ADIMVTGTVDGWRKIAKDEGAKAFKFGAMSNVLRGMGAFVLYDEIKKYV 297
Db 247 KGKEIQYKNTIDCWIKILRNDEGFGFEGKAMANYIRGAGGALVLFYDELQKLI 301

Search completed: November 12, 2002, 16:48:36
Job time : 14.9686 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:20 : Search time 7.6495 Seconds

(without alignments)
1610.364 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGVA...LRMGARVLYDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526.5	98.3	298	ADP1_HUMAN	P12235 ratu
2	1466.5	94.4	298	ADP1_RAT	Q05622 ratu
3	1463.5	94.2	298	ADP1_MOUSE	P48962 mus
4	1453.5	93.6	297	ADP1_BOVIN	P02722 bos
5	1408.5	90.7	298	ADP2_MOUSE	P51881 mus
6	1407.5	90.6	298	ADP2_RAT	Q09673 ratu
7	1398.5	90.1	298	ADP2_HUMAN	P05141 homo
8	1385.5	89.2	298	ADP3_HUMAN	P12236 homo
9	1380.5	88.9	298	ADP3_BOVIN	P32007 bos
10	1211	78.0	297	ADP1_DROME	Q26365 dros
11	1162.5	74.9	301	ADP1_ANGCA	Q27238 anop
12	973.5	62.7	339	ADP1_CHIK	P31692 chlo
13	770.5	45.6	308	ADP1_CHIK	P27080 chl
14	756.5	48.7	387	ADP1_MAIZE	P04709 zea
15	752.5	48.5	322	ADP1_SCHPO	Q09188 sch
16	752.5	48.4	382	ADP1_GOSHI	Q22342 gos
17	751.5	48.4	382	ADP1_ORYSA	P31691 ory
18	751.5	48.4	382	ADP2_MAIZE	P12857 zea
19	746.5	48.0	381	ADP1_ARATH	P31167 ara
20	744.5	47.9	386	ADP1_SOLTU	P25083 sol
21	742.5	47.8	331	ADP1_WHEAT	Q41629 trit
22	740	47.6	386	ADP2_SOLTU	P27081 sol
23	736	47.4	307	ADP3_YEAST	P18238 sac
24	734	47.3	318	ADP2_YEAST	P18239 sac
25	733.5	47.2	313	ADP1_NEUCR	P02723 neu
26	731	47.1	385	ADP2_ARATH	P40941 ara
27	729	46.9	305	ADP1_KLULA	P49382 kli
28	728.5	46.9	331	ADP2_WHEAT	Q41630 trit
29	718.5	46.3	309	ADP1_YEAST	P04710 sac
30	302.5	19.5	678	CMC1_HUMAN	O75446 homo
31	300.5	19.3	330	GDC_BOVIN	O01888 bos
32	296.5	19.1	702	CMC1_CAEL	O21153 cae
33	296	19.1	588	CMC2_CAEL	O20799 cae

ALIGNMENTS

RESULT 1	ADP1_HUMAN	STANDARD:	PRT:	298 AA.
AC	P12235;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1).			
GN	SLC25A4 OR ANT1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
NP	SEQUENCE FROM N.A.			
RA	MEDLINE=89236396; PubMed=2541251;			
RT	Cozens A.L., Runswick M.J., Walker J.E.;			
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";			
RL	J. Mol. Biol. 206:261-280(1989).			
RN	[2]			
NP	SEQUENCE FROM N.A.			
RA	MEDLINE=89340499; PubMed=2547778;			
RT	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.;			
RT	Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;			
RT	"A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed.";			
RL	J. Biol. Chem. 264:13998-14004(1989).			
RN	[3]			
NP	SEQUENCE FROM N.A.			
RA	MEDLINE=88041149; PubMed=2823266;			
RT	Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;			
RT	"cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).			
RN	[4]			
NP	SEQUENCE FROM N.A.			
RA	TISSUE-Eye;			
RC	Strausberg R.;			
RL	Submitted (May-2001) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
NP	SEQUENCE OF 1-37 FROM N.A.			
RA	TISSUE-Liver;			
RC	MEDLINE=88124845; PubMed=2829183;			
RT	Houdsworth J., Attardi G.;			
RT	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).			
RN	[6]			
NP	VARIANTS PRO PRO-114 AND MET-289.			
RA	MEDLINE=20385067; PubMed=10926541;			
RT	Kauonen J., Juselius J.K., Tiranli V., Kytala A., Zeviani M.,			
RT	Comi G.P., Keranen J., Peltonen L., Suomalainen A.;			
RT	"Role of adenine nucleotide translocator 1 in mtDNA maintenance.";			

P16261 ratu mus norv
Q99297 saccharomyc
P16260 homo sapien
Q9150 homo sapien
Q19529 caenorhabd1
Q912d1 homo sapien
Q9qxx4 mus musculi
Q9h1K4 homo sapien
Q922b2 mus musculi
Q03028 saccharomyc
Q95258 homo sapien
Q9va73 drosophila

```

RL Science 289:782-785(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
CC progressive external ophthalmoplegia with various mitochondrial
CC DNA deletions (PEO). Patients with PEO have mitochondrial
CC myopathy, progressive external ophthalmoplegia, and other
CC abnormalities associated with multiple different deletions of
CC mitochondrial DNA.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J02956; AAA61223.1; -
DR EMBL: J03593; AAA36751.1; -
DR EMBL: J04982; AAA51736.1; -
DR EMBL: BC008664; AAH08664.1; -
DR PIR: A28116; A28116.
DR PIR: A39891; A39891.
DR PIR: S03893; S03893.
DR PIR: A44778; A44778.
DR Genew; HGNC:10990; SLC25A4.
DR MIM; 103220; -
DR MIM; 157640; -
DR InterPro: IPR002067; Mito_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCH_CARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Disease mutation.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
FT VARIANT 114 114 A -> P (IN PEO).
FT VARIANT 289 289 /FTID-VAR_012111.
FT VARIANT 289 289 V -> M (IN PEO).
FT CONFLICT 16 16 G -> A (IN REF. 3).
FT CONFLICT 147 149 KGA -> RR (IN REF. 3).
FT CONFLICT 227 227 V -> L (IN REF. 3).
SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAC4E7CEFB CRC64;

Query Match 98.3%; Score 1526.5; DB 1; Length 298;
Best Local Similarity 98.3%; Pred. No. 2; 3e-132;
Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGDIAWSFLDDELGAVAANAASKTAVAPIEVEKLLQVHSAKQISAERKQGIITDCVVR 60
DB 1 MGDIAWSFLDDELGAVAANAASKTAVAPIEVEKLLQVHSAKQISAERKQGIITDCVVR 60
QY 61 IPKEGFLSEWRGNLANVIRYPTQALNFAFKRKYKQLFLGVDVRHROFWRYFAGNLASG 120
DB 61 IPKEGFLSEWRGNLANVIRYPTQALNFAFKRKYKQLFLGVDVRHROFWRYFAGNLASG 120
QY 121 GAAGATSLCFYPLDFAFRTLAADVGR-RAQREHFGJGDCITIKFKSDGLGLYQGFNV 179
DB 121 GAAGATSLCFYPLDFAFRTLAADVGR-RAQREHFGJGDCITIKFKSDGLGLYQGFNV 179

```

```

DB 121 GAAGATSLCFYPLDFAFRTLAADVGRGAAGREFHGLGDCITIKFKSDGLGLYQGFNV 180
QY 180 VQGIITRYAAAFYGYDPAKGMIPDKNVHIFVSMIAQSYAVAGLSYFPDYRRMM 239
DB 181 VQGIITRYAAAFYGYDPAKGMIPDKNVHIFVSMIAQSYAVAGLSYFPDYRRMM 240
QY 240 QSGRRGADIMYTGVDWCRKIAKDEGAKAFKKGAMSVNLKMGAFVLYDEIKKYV 297
DB 241 QSGRRGADIMYTGVDWCRKIAKDEGAKAFKKGAMSVNLKMGAFVLYDEIKKYV 298

RESULT 2
ADT1_RAT
ID ADT1_RAT STANDARD; PRT; 298 AA.
AC Q05962;
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 40, Last annotation update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinozaki Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
CC EXTENT, IN BRAIN AND KIDNEY.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X61667; CAA43842.1; -
DR EMBL: D12770; BAA02237.1; -
DR InterPro: IPR002067; Mito_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCH_CARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6BC320 CRC64;

Query Match 94.4%; Score 1466.5; DB 1; Length 298;
Best Local Similarity 94.3%; Pred. No. 7e-127;

```

Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAKQYKGIIDCVYR 60
 DB 1 MGDALSLFKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAKQYKGIIDCVYR 60

QY 61 IPKEGFLSPFRGNLANIYRFFPTQALNFAFKDKYKQFLGVDNRHKQFMYFAGNLASG 120
 DB 61 IPKEGFLSPFRGNLANIYRFFPTQALNFAFKDKYKQFLGVDNRHKQFMYFAGNLASG 120

QY 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAOREPHGLDCCIIRKFSKGLKGLYOGFNV 179
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAOREPHGLDCCIIRKFSKGLKGLYOGFNV 179

QY 180 VOGIIIRAAAFGYVDYAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTDYVRRMM 239
 DB 181 VOGIIIRAAAFGYVDYAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTDYVRRMM 240

QY 240 QSGRKGADIMYTGTCWRKIAKDEGAKAFKFGAMSNVLRMGAFVLYVDEIKKYV 297
 DB 241 QSGRKGADIMYTGTCWRKIAKDEGAKAFKFGAMSNVLRMGAFVLYVDEIKKYV 298

RESULT 3
 ADT1_MOUSE
 ID ADT1_MOUSE STANDARD: PRT: 298 AA.
 AC PA8962: 062164;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).
 GN SIC25A4 OR ANTI OR ANCI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse homologs.";
 RT Mamm. Genome 7:25-30(1996).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=Muscle;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Eye;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).

CC -----
 CC DR EMBL; U27315; AAC52837.1; -;
 CC DR EMBL; X74510; CAAS2616.1; -;
 CC DR EMBL; AF240002; AAF64470.1; -;
 CC DR EMBL; BC003791; AAH03791.1; -;
 CC DR EMBL; BC026925; AAH26925.1; -;
 CC DR MGI; MGI:1353495; SIC25a4.
 CC DR InterPro; IPR002067; Mit_carrier.
 CC DR InterPro; IPR001993; Mitoch_carrier.
 CC DR Pfam; PF00153; mito_carr; 3
 CC DR PRINTS; PR00926; MITOCARRIER.
 CC DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 CC KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 CC KW Multigene family.
 CC FT TRANSMEM 12 29 1 (POTENTIAL).
 CC FT TRANSMEM 73 91 2 (POTENTIAL).
 CC FT TRANSMEM 117 134 3 (POTENTIAL).
 CC FT TRANSMEM 176 195 4 (POTENTIAL).
 CC FT TRANSMEM 214 231 5 (POTENTIAL).
 CC FT TRANSMEM 273 291 6 (POTENTIAL).
 CC FT REPEAT 1 110 1.
 CC FT REPEAT 111 208 2.
 CC FT REPEAT 209 298 3.
 CC FT CONFLICT 136 136 F->L (IN REF. 1).
 CC SQ SEQUENCE 298 AA; 32904 MW; 3A849FEB0981462 CRC64;

Query Match 94.2%; Score 1463.5; DB 1; Length 298;
 Best Local Similarity 94.0%; Pred. No. 1.3e-126;
 Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAKQYKGIIDCVYR 60
 DB 1 MGDALSLFKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAKQYKGIIDCVYR 60

QY 61 IPKEGFLSPFRGNLANIYRFFPTQALNFAFKDKYKQFLGVDNRHKQFMYFAGNLASG 120
 DB 61 IPKEGFLSPFRGNLANIYRFFPTQALNFAFKDKYKQFLGVDNRHKQFMYFAGNLASG 120

QY 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAOREPHGLDCCIIRKFSKGLKGLYOGFNV 179
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAOREPHGLDCCIIRKFSKGLKGLYOGFNV 180

QY 180 VOGIIIRAAAFGYVDYAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTDYVRRMM 239
 DB 181 VOGIIIRAAAFGYVDYAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTDYVRRMM 240

QY 240 QSGRKGADIMYTGTCWRKIAKDEGAKAFKFGAMSNVLRMGAFVLYVDEIKKYV 297
 DB 241 QSGRKGADIMYTGTCWRKIAKDEGAKAFKFGAMSNVLRMGAFVLYVDEIKKYV 298

RESULT 4
 ADT1_BOVIN
 ID ADT1_BOVIN STANDARD: PRT: 297 AA.
 AC P02722;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP carrier protein, heart isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SIC25A4 OR ANTI.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89229093; PubMed=2540808;
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;

```

RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues."
RL Biochemistry 28:866-873(1989).
RP [2]
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aguilu H., Misra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria."
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence."
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13783; AAA0363.1; -.
DR EMBL: M24102; AAA30768.1; -.
DR PIR: A03181; XMO.
DR PIR: A24822; A24822.
DR PIR: A43646; A43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondonid; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;

Query Match 93.6%; Score 1453.5; DB 1; Length 297;
Best Local Similarity 94.6%; Pred. No. 11e-125;
Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

```

```

DB 122 AGATSLCFYPLDFAFRTLAADVGAQAQREFTGLNCITKIFKSDGLGLYGFNVSVQ 181
OY 182 GIITVRAAFYGYDPAKGLPDPKVNHTFVSMIAOSYAVAGLSYEDVRRMMMS 241
DB 182 GIITVRAAFYGYDPAKGLPDPKVNHTFVSMIAOSYAVAGLSYEDVRRMMMS 241
OY 242 GRRKADIMYGTVDGWRKIAKDEGAKAFKGAWSNVLRMGAFVLYVDEIKRYV 297
DB 242 GRRKADIMYGTVDGWRKIAKDEGAKAFKGAWSNVLRMGAFVLYVDEIKRYV 297

RESULT 5
ADT2_MOUSE STANDARD: PRT: 298 AA.
ID ADT2_MOUSE
AC P51881; 061311;
DT 01-OCT-1996 (Rel. 34, created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs."
RL Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Costet P., Laplace C.;
RL Submitted (Feb-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP REVISIONS.
RA Laplace C.;
RL Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20432087; PubMed=10974536;
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes."
RL Gene 254:57-66(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27316; AAC52838.1; -.
DR EMBL: U10404; AAA19009.1; -.
DR EMBL: X70847; CAA50196.1; -.

```

DR EMBL: AF240003; AAF64471.1; -
DR MGD: MG1:1353496; S1C25A5.
DR InterPro: IPR002067; Mito_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER.
DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SO SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;

Query Match 90.7%; Score 1408.5; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 1.4e-121;
Matches 266; Conservative 17; Mismatches 13; Indels 1; Gaps 1;

QY 1 MGDHASFLLKDFLAGVAAVASTAVAPTERVYKLLQVGHASQISAEQYKGIIDCVVR 60
DB 1 MTDAAVSFAKDFLAGVAAVASTAVAPTERVYKLLQVGHASQISAEQYKGIIDCVVR 60
QY 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQLFSGVDRHKQFWRYPAGNLAGS 120
DB 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQLFSGVDRHKQFWRYPAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFHGLGDCIIRKFSKDLRGLGYGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFHGLGDCIIRKFSKDLRGLGYGFNVS 179
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFHGLGDCIIRKFSKDLRGLGYGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFHGLGDCIIRKFSKDLRGLGYGFNVS 180
QY 180 VGGIITRYRAAYFGVYDTAGMLPDPKNVHIFVSWMTAOSTVAVAGLSTPFDVRRRM 239
DB 181 VGGIITRYRAAYFGVYDTAGMLPDPKNVHIFVSWMTAOSTVAVAGLSTPFDVRRRM 240
QY 240 QSGRKADIMYGTGTCVDCWKRIADDEGAKAFKGCAMSNVLRMGAGVLLVLYDEIKRY 296
DB 241 QSGRKADIMYGTGTCVDCWKRIADDEGAKAFKGCAMSNVLRMGAGVLLVLYDEIKRY 297

RESULT 6
ADT2_RAT STANDARD; PRT; 298 AA.
AC 009073;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rurinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN: Sprague-Dawley; TISSUE: liver;
RX MEDLINE: 94002161; PubMed: 8399300;
RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
encoding rat mitochondrial adenine nucleotide translocator";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND

CC SKELETAL MUSCLE.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D12771; BA02238.1; -
DR InterPro: IPR002067; Mito_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER.
DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SO SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;

Query Match 90.6%; Score 1407.5; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 1.7e-121;
Matches 266; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 1 MGDHASFLLKDFLAGVAAVASTAVAPTERVYKLLQVGHASQISAEQYKGIIDCVVR 60
DB 1 MTDAAVSFAKDFLAGVAAVASTAVAPTERVYKLLQVGHASQISAEQYKGIIDCVVR 60
QY 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQLFSGVDRHKQFWRYPAGNLAGS 120
DB 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQLFSGVDRHKQFWRYPAGNLAGS 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFHGLGDCIIRKFSKDLRGLGYGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFHGLGDCIIRKFSKDLRGLGYGFNVS 180
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFHGLGDCIIRKFSKDLRGLGYGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFHGLGDCIIRKFSKDLRGLGYGFNVS 180
QY 180 VGGIITRYRAAYFGVYDTAGMLPDPKNVHIFVSWMTAOSTVAVAGLSTPFDVRRRM 239
DB 181 VGGIITRYRAAYFGVYDTAGMLPDPKNVHIFVSWMTAOSTVAVAGLSTPFDVRRRM 240
QY 240 QSGRKADIMYGTGTCVDCWKRIADDEGAKAFKGCAMSNVLRMGAGVLLVLYDEIKRY 296
DB 241 QSGRKADIMYGTGTCVDCWKRIADDEGAKAFKGCAMSNVLRMGAGVLLVLYDEIKRY 297

RESULT 7
ADT2_HUMAN STANDARD; PRT; 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: Placenta;

RX MEDLINE=90375457; PubMed=2168878;
 RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurtzel J.;
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular
 cloning and sequence.";
 RL J. Biol. Chem. 265:16060-16063(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87166056; PubMed=3031073;
 RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
 RA Baserga R.;
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
 growth-regulated.";
 RL J. Biol. Chem. 262:4355-4358(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chen C.N., Su Y., Bayhayan P., Siruno A., Nagaraja R.,
 RA Mazarella R.A., Schlessinger D., Chen E.Y.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Becker M., Graves T., Ozersky P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 47-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M57424; AAA51737.1; -;
 DR EMBL: J02683; AAA35579.1; -;
 DR EMBL: L78810; AAB39266.1; -;
 DR EMBL: AC004000; AAB96347.1; -;
 DR EMBL: J03591; AAA36749.1; -;
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR Genew; HGNC:10991; SLC25A5.
 DR MIM; 300150; -;
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).

FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;
 Query Match 90.1%; Score 1398.5; DB 1; Length 298;
 Best Local Similarity 88.9%; Pred. No. 1,2e-120;
 Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;
 QY 1 MGDHMSFLDPLAGAAVAASKTAAPVIRVKLLLOVHASQISAEKKGKIIICVVR 60
 DB 1 MTDAAVSFAKDFLAGVAAAIKTAAPVIRVKLLLOVHASQITADKQYKGIICVVR 60
 QY 61 IPKEGFLSFWRGNLANVIRYFPPTALNFAFKDKYKOLFGLGVDRHKEFRYFAGNLSAG 120
 DB 61 IPKEGVLSTWRGNLANVIRYFPPTALNFAFKDKYKOLFGLGVDRHKEFRYFAGNLSAG 120
 QY 121 GAAGATSLCEVYPLDFARTLADVCGRR-AQREFHGLGDCIIFKFSQDGLRGLYQGFNVS 179
 DB 121 GAAGATSLCEVYPLDFARTLADVCGRR-AQREFHGLGDCIIFKFSQDGLRGLYQGFNVS 180
 QY 180 VGGITIRAAVFGYDFAKGLMDPKNVHIFVSMITAOVSATAVAGLSTPFDVRRRMM 239
 DB 181 VGGITIRAAVFGYDFAKGLMDPKNVHIFVSMITAOVSATAVAGLSTPFDVRRRMM 240
 QY 240 QSGRKGADIMYGTVDCKRIADDEGAKAFKGAWSNVLRMGAFVLYLDEIKRY 296
 DB 241 QSGRKGADIMYGTVDCKRIADDEGAKAFKGAWSNVLRMGAFVLYLDEIKRY 297
 RESULT 8
 ADT3_HUMAN STANDARD; PRT; 298 AA.
 ID ADT3_HUMAN
 AC P12336; Q96C49;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
 GN (Adenine nucleotide translocator 3) (ANT 3).
 DE SLC25A6 OR ANT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
 RA Margolin J.F.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain; Cervix; Eye; and Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.

[illegible]

QY 240 QSGRRGADIMYGTGVDCKRIKADGAKAFKAGMSNVLRGMSGAFVLVYDEIKKYV 297
 ID_1DROME STANDARD; PRT; 297 AA.
 AC Q26365; Q26254; P91614; G9V270;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 translocator) (ANT) (Stress sensitive B protein).
 GN SESB OR A/A-T OR CG16944.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92389367; PubMed=1387687;
 RA Louvi A., Tsilioni S.G.;
 RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
 RT melanogaster shows a high degree of similarity with the mammalian
 RT ADP/ATP translocases."
 RL J. Mol. Evol. 35:44-50(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94350065; PubMed=7520869;
 RA Hutter P., Karch F.;
 RT "Molecular analysis of a candidate gene for the reproductive
 RT isolation between sibling species of Drosophila."
 RL Experientia 50:749-762(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RA Zhang Y.Q., Davis A.W., Roote J., Hermann S., Ashburner M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Paulos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodier A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Hartvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaisl M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson C.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson S.D., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: S43651; AAB23114.1; -;
 DR EMBL: S71762; AAB31734.3; -;
 DR EMBL: Y10618; CAAT1628.1; -;
 DR EMBL: AE003484; AAF47957.1; -;
 DR FlyBase: FBgn0003360; sesb.
 DR InterPro: IPR002067; MLC_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carri; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 177 196 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 272 290 6 (POTENTIAL).
 FT TRANSMEM 18 19 QV -> GI (IN REF. 3 AND 4).
 FT TRANSMEM 81 81 I -> Y (IN REF. 1).
 FT TRANSMEM 200 200 R -> RG (IN REF. 3 AND 4).
 FT TRANSMEM 266 266 G -> A (IN REF. 2).
 FT TRANSMEM 267 268 PC -> TGA (IN REF. 3 AND 4).
 FT TRANSMEM 268 268 C -> S (IN REF. 1).
 SQ SEQUENCE 297 AA; 32880 MM; AA639439968F9750 CRC64;
 Query Match 78.0%; Score 1211; DB 1; Length 297;
 Best Local Similarity 79.4%; Pred. No. 1,6e-103;
 Matches 231; Conservative 25; Mismatches 33; Indels 2; Gaps 2;
 QY 5 AWSFLKDFLAGAANAASKTAVADIERYKLLLYOHASKQDISAEKQYKGIIDCVRIKPE 64
 DB 7 AVGVKDFPAAGQVSAASKTAVADIERKLLLYOHISKQISPKQYKGMWDCFIIRIPE 66
 QY 65 OGFLSPFNGNLANITREFFPTQALNFAFKDKYKQFLGVDYDHKQFWMYFNGNLASGAAG 124
 DB 67 OGFSFSGNLANITREFFPTQALNFAFKDKYKQFLGVDYDHKQFWMYFNGNLASGAAG 126
 QY 125 ATSLCFVYPLDFAFRTPLAADVGRRAOREFHGLGDCIIRIKFSDGLRGLYGFNFVYOGII 184
 DB 127 ATSLCFVYPLDFAFRTPLAADVGRRAOREFHGLGDCIIRIKFSDGLRGLYGFNFVYOGII 186
 QY 185 TYRAVFGVDTAKGMLDPKRNVIHFWSMITAGSVTAAGLSYPPDTVRRMMQSGRK 244
 DB 187 TYRAVFGVDTAKGMLDPKRNVIHFWSMITAGSVTAAGLSYPPDTVRRMMQSGRK 245
 QY 245 GADIMYGTGVDCKRIKADGAKAFKAGMSNVLRGMSGAFVLVYDEIKKYV 295
 DB 246 ATEVIYKNTLHCWATIAKQEG-PCFFGAGAFSNILRGTCGAFVLVYDEIKKYV 295

RESULT 11

ID	ADT_ANOGA	STANDARD:	PRT:	301 AA.
AC	027238:			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).			
OS	Anopheles gambiae (African malaria mosquito).			
OC	Eukaryota: Metazoa: Arthropoda: Mandibulata: Pancrustacea: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Nematocera: Culicoidae: Anopheles.			
OX	NCBI_TaxID=7165;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-G3:			
RX	MEDLINE-94348635; PubMed-8069414;			
RA	Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;			
RT	"A CDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae."			
RL	Insect Mol. Biol. 3:35-40(1994).			
CC	- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.			
CC	- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.			
CC	- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.			
CC	- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).			
CC	or send an email to license@sib-sib.ch).			
CC	EMBL: L11618; AAB04104.1; -			
DR	EMBL: L11617; AAB04105.1; -			
DR	InterPro: IPR002067; Mit_carr.			
DR	InterPro: IPR001993; Mitoch_carr.			
DR	Pfam: PF00153; mito_carr.3			
DR	PRINTS: PR00926; MITOCARRIER.			
DR	PROSITE: PS00215; MITOCH_CARRIER; 3.			
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.			
FT	TRANSMEM 14 31 1 (POTENTIAL).			
FT	TRANSMEM 75 93 2 (POTENTIAL).			
FT	TRANSMEM 119 136 3 (POTENTIAL).			
FT	TRANSMEM 178 197 4 (POTENTIAL).			
FT	TRANSMEM 216 233 5 (POTENTIAL).			
FT	TRANSMEM 275 293 6 (POTENTIAL).			
SEQUENCE	301 AA: 32863 MW; 4CC9E17C9F8DA08B CRC64:			

Query Match

Best Local Similarity 74.9%; Score 1162.5; DB 1; Length 301;

Matches 223; Conservative 26; Mismatches 90; Indels 1; Gaps 1;

RESULT 12

ID	ADT_CHLKE	STANDARD:	PRT:	339 AA.
AC	P31692:			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).			
OS	Chlorella kessleri.			
OC	Eukaryota: Viridiplantae: Chlorophyta: Trebouxiophyceae: Chlorellales: Chlorellaceae: Chlorella.			
OX	NCBI_TaxID=3074;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-92084708; PubMed-1748677;			
RA	Hilgarth C., Sauer N., Tanner W.;			
RT	"Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella."			
RL	J. Biol. Chem. 266:24044-24047(1991).			
CC	- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.			
CC	- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.			
CC	- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.			
CC	- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).			
CC	or send an email to license@sib-sib.ch).			
CC	EMBL: M76669; AAA33027.1; -			
DR	PIR: A41677; A41677.			
DR	InterPro: IPR002067; Mit_carr.			
DR	InterPro: IPR001993; Mitoch_carr.			
DR	Pfam: PF00153; mito_carr.3.			
DR	PRINTS: PR00926; MITOCARRIER.			
DR	PROSITE: PS00215; MITOCH_CARRIER; 3.			
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.			
FT	TRANSMEM 45 62 1 (POTENTIAL).			
FT	TRANSMEM 108 126 2 (POTENTIAL).			
FT	TRANSMEM 151 168 3 (POTENTIAL).			
FT	TRANSMEM 209 228 4 (POTENTIAL).			
FT	TRANSMEM 248 265 5 (POTENTIAL).			
FT	TRANSMEM 304 322 6 (POTENTIAL).			
SEQUENCE	339 AA: 36686 MW; 54779734A33B3942 CRC64:			

Query Match

Best Local Similarity 62.7%; Score 973.5; DB 1; Length 339;

Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;

```

Db 159 AGSLILVPLDFAFRTRLAADVCGSKSREFGLDCLSKVYKRGCPMALYCGFVSQGI 218
Qy 185 IYSAAYGVYDFTAKML-PDPKNVHIFVSMIAOSVTAVAGLSYDPDYRRRRMMQSGR 243
Db 219 VYGAATFGLDTRAKGVLEKERTANFPAKWAQAVTAGAGVLSYDPDYRRRLMQS-- 276
Qy 244 KGADIMYTGTVDCMRKIADKDEGAKAFKFGAMSVNLKMGAFVLYLDEIKKYV 297
Db 277 -GGERQYNGTIDCMRKRYAQEGMKAFKFGAMSVNLGAGGAFVLYLDEIKKFI 329

RESULT 13
ADT_CHLRE STANDARD; PRT; 308 AA.
AC P27080;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
GN ABT.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=FUDA4-R2;
RX MEDLINE=93204887; PubMed=8455552;
RA Sharpe J.A., Day A.;
RT Structure, evolution and expression of the mitochondrial ADP/ATP
translocator gene from Chlamydomonas reinhardtii.";
RL Mol. Genet. 237:134-144(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL: X65194; CAA46311.1; -
CC PIR: S30259; S30259.
CC InterPro: IPR002067; MitoCarrier.
CC InterPro: IPR001993; MitoChCarrier.
CC Pfam: PF00153; MitoCarrier.
CC PRINTS: PR00926; MITOCHARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 74 92 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 234 251 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
SQ SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;

Query Match 49.6%; Score 770.5; DB 1; Length 308;
Best Local Similarity 52.6%; Pred. No. 3,4e-63;
Matches 159; Conservative 49; Mismatches 77; Indels 17; Gaps 6;
Qy 7 SFLKDFLAGAANAASVTAAPIERVKLLIQV-HASKQISAQKQYGIIDCVIRIKEQ 65
Db 7 NFWVDPLAGLSAASVSTAAPIERVKLLIQNDEMIRKGLASPKYIGECFVIRVEE 66

```

```

Qy 66 GFLSFWRGNLANIYRFPYQALNFAFKDKYKQFLGVDVRHKOFWRYFAGNLASGAGA 125
Db 67 GFQSLRGNNTANIRYFPPQALNFAFKDKRNF--GFNKDKRYKMFPGNMASGAGA 124
Qy 126 TSLCEVYPLDFAFRTRLAADVGR---ADREFGLDCLIKFKPSGLRGLYGFVNSVQ 181
Db 125 VSLSPYSLIDYARTRLANDAKSAKKGAGDQFNGLDVYVRKTIASDGIAGLYRGNISCV 184
Qy 182 GIIYRAAYGVYDFTAKG-MLPDPKNVHIFVSMIAOSVTAVAGLSYDPDYRRRRMMQ 240
Db 185 GIIVYRGLIFGMDSLKPVVGLVGLANNFLAFLGLMGTIGAGLSYPLDITRRMMMT 244
Qy 241 SGRKGADIMYTGTVDCMRKIADKDEGAKAFKFGAMSVNLKMGAFVLYLDEI-----K 294
Db 245 S--GSAVKYNSHFQGEIVKNEGKSLFKGAGANILRAVAGVLAGDQLQVILLCK 301
Qy 295 KY 296
Db 302 KY 303

RESULT 14
ADT_MAIZE STANDARD; PRT; 387 AA.
ID ADT1_MAIZE
AC P04709;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein 1, mitochondrial precursor (ADP/ATP
translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN ANT1 OR ANT-G1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MUTIND-FR7205034;
RX MEDLINE=91322533; PubMed=1863785;
RA Winung B.M., Day C.D., Sarah C.J., Leaver C.J.;
RT "Nucleotide sequence of two cDNAs encoding the adenine nucleotide
translocator from Zea mays L.";
RL Plant Mol. Biol. 17:305-307(1991).
RN [2]
RP SEQUENCE OF 59-387 FROM N.A.
RC STRAIN-CV. B37N;
RX MEDLINE=8938399; PubMed=2547608;
RA Leaver C.J., Bathgate B., Baker A.;
RT "Two genes encode the adenine nucleotide translocator of maize
mitochondria. Isolation, characterisation and expression of the
structural genes.";
RL Eur. J. Biochem. 183:303-310(1989).
RN [3]
RP SEQUENCE OF 70-387 FROM N.A.
RX MEDLINE=8529781; PubMed=2994015;
RA Baker A., Leaver C.J.;
RT "Isolation and sequence analysis of a cDNA encoding the ATP/ADP
translocator of Zea mays L.";
RL Nucleic Acids Res. 13:5857-5867(1985).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@lsb.sib.ch).

DR EMBL: X57556; CAA40781.1; -;
DR EMBL: X15711; CAA33742.1; -;
DR EMBL: X02842; CAA26600.1; -;
DR PIR: A24072; A24072.
DR PIR: S05199; S05199.
DR PIR: S14876; S14876.
DR MatzEBD: I7145; -;
DR InterPro: IPRO02067; Mit_carrier.
DR InterPro: IPRO01993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
FT TRANSIT 1 77
FT CHAIN 1 77
FT TRANSMEM 78 387
FT TRANSMEM 91 108
FT TRANSMEM 153 171
FT TRANSMEM 196 213
FT TRANSMEM 257 276
FT TRANSMEM 296 313
FT TRANSMEM 352 370
FT CONFLICT 102 102
FT CONFLICT 154 154
SQ SEQUENCE 387 AA; 42391 MW; DE73BDF47BD57D CRC64;
Query Match Best Local Similarity 48.7%; Score 756.5; DB 1; Length 387;
Matches 164; Conservative 41; Mismatches 77; Indels 23; Gaps 7;
QY 7 SELDLFLAGAAVAANSKRAVAPIERVKLLIQV-Q-HASKQISAEKKYKGIGDCVAVLPKEQ 65
Db ::::|||||:|||||||:|||||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
66 GFLEFWRGNLANVRIEPTQAENFAFKDKRYOLFVGVDVRHKOFRPFIAGNLAASGAGA 125
Db NFMIDPMFGVSAASAKTPAAPIERVKLLIONODEMISGRUSEPKGVDFCKTIDE 145
146 GFSSLMRGNTANVRIEPTQALNFARFYKRLFNFKKDR-DGYKKMFAGNLASGAGA 204
QY 126 TSLCEPVLDPAARRPLADVGR--AOREFHGLDCIIIFKSQSLGKLTVGFENVVOG 182
Db :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
205 SLSFEFVSLDAFRRLLANDAKAAKGGGEKOFELDVARYKTLSGIGLVYRGENFINSYG 264
QY 183 IIRRAAFEGVYDNK----GMLEDPKNVHFVSMTIAQSSTVAAYAGLSYEPFDIVRRM 237
Db |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
265 IIVRGILYGLYDSIKRPVLVTGNLOD---NFFASFALGMLITNGAGLASPIDIVRRRM 320
QY 238 MMOSGRKADIMITYGTVDCKMRKIADDEGAKAFFKAGWNSVLKMGCAFVLYLDEI--- 293
Db |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
321 MMTSGEA---VKYKSSLDAFOOIEKKESPSLFKAGANIIRAIGAGVLSGYDQLQILE 377
QY 294 --KKY 296
Db |||
Db 378 FGKRY 382
RESULT 15
ADLT_SCHPO ID ADLT_SCHPO STANDARD: PRT: 322 AA.
AC Q09188;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide
DE translocator) (ANT).
GN ANCI OR SPBC530.10C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.

Query Match 48.5%; Score 752.5; DB 1; Length 322;

Query Match	48.5%	Score 752.5	DB 1	Length 322
0X	NCBI_TaxID=4896;			
1P	SEQUENCE FROM N.A.			
1P	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RX	MEDLINE=96257204; PubMed=6675018;			
RA	Cozlin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;			
RT	"Cloning of the gene encoding the mitochondrial adenine nucleotide			
RT	carrier of Schistoscharyomycs pombe by functional complementation in			
RL	Saccharomyces cerevisiae.";			
RL	Gene 171:113-117(1996).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RX	MEDLINE=21848401; PubMed=11859360;			
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,			
RA	Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,			
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,			
RA	Collins M., Connor R., Cronin A., Davis P., Felkewell T., Fraser A.,			
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,			
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jags K.,			
RA	James K., Jones L., Jones M., Leuther S., McDonald S., McLean C.,			
RA	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,			
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,			
RA	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,			
RA	Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,			
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,			
RA	Woodward J., Voicakeert G., Aert R., Robben J., Glymptiez B.,			
RA	Welters I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,			
RA	Gabel C., Fuchs M., Ertz C., Holzer E., Moesti D., Hilbert H.,			
RA	Bozsym K., Langier I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,			
RA	Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,			
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaune V., Mottier S.,			
RA	Gallberg F., Aves S.J., Xiang Z., Hunt C., Moore K., Hunt S.M.,			
RA	Lucas M., Rochet M., Galliard C., Tallade V.A., Garzon A., Thode G.,			
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,			
RA	Domínguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,			
RA	Cerruti L., Lowe T., McCombie W.R., Paulsen I., Polishkin J.,			
RA	Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;			
RL	"The genome sequence of Schistoscharyomycs pombe.";			
RL	Nature 415:871-880(2002).			
CC	-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE			
CC	MITOCHONDRIAL INNER MEMBRANE.			
CC	-I- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial			
CC	inner membrane.			
CC	-I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.			
CC	-I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on ways			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; Z49974; CAA90275.1; -			
DR	EMBL; AL023634; CAA19176.1; -			
DR	InterPro; IPR002067; Mit_carrier.			
DR	InterPro; IPR001993; Mitoch_carrier.			
DR	Pfam; PF00153; mito_carr; 3			
DR	PRINTS; PR00926; MITOCARRIER.			
DR	PROSITE; PS00215; MITOCH_CARRIER; 2.			
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.			
FT	TRANSMEM 28 48 1 (POTENTIAL).			
FT	TRANSMEM 93 111 2 (POTENTIAL).			
FT	TRANSMEM 131 151 3 (POTENTIAL).			
FT	TRANSMEM 197 217 4 (POTENTIAL).			
FT	TRANSMEM 222 242 5 (POTENTIAL).			
FT	TRANSMEM 289 309 6 (POTENTIAL).			
SO	SEQUENCE 322 AA; 35020 MW; BAC3D16A0F41AFC CRC64;			

Best Local Similarity 52.9%; Pred. No. 1.6e-61;
Matches 156; Conservative 51; Mismatches 75; Indels 13; Gaps 6;
QY 7 SFLKDFLAGAVAAAVSKTAAVAPIERVKLLQOVHASKOISAEK--OYKGIIDCVVRIPK 63
Db 26 TFFEDFMGGVSAVSAVSKTAAAPIERVKLLIQN--DEMIRAGRLSHRYKGI GECFKRTAA 83
QY 64 EQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGVDNRHKQFWRRYFAGNLAGGAA 123
Db 84 EEGVYISLMRGNTANVLRFFPTQALNFAFKDKFKMF--GYKKERDGYAKMFAGNLAGGAA 142
QY 124 GATSLCFVYPLDFARTRLAAD--VGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
Db 143 GAASLLEFVYSLDYARTRLANDAKSARKGGERQFNGLVYRKYRSDGLRGLYRGFGPSV 202
QY 181 QGIIYRAAYFGVYDTAKG--MLPDPKNVHIFVSMIAOSVTAAGLLSYPEDTVRRRMM 239
Db 203 VGIIVYRGLYFGMYDTLKPVYLVGPLEGNFLASFLLGMAVYTGSGVASYPDLDTIRRRMM 262
QY 240 QSGRRGADIMYGTGDCWRKIADDEGAKAFEFKAMSNVLRGMGAFVLYLYDEIK 294
Db 263 TSGEA--VKYSSSECGRQILAKEGARSFPEKAGANILRGVAGAGVLSIYDQVQ 314

Search completed: November 12, 2002, 16:46:26
Job time : 8.6495 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:45 : Search time 25.2766 Seconds
(without alignments)
2421.054 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVAAA.....LRGMGAFVLYLDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1464.5	94.3	298	6	046373	046373 Oryctolagus
2	1463.5	94.2	298	11	062164	062164 mus musculus
3	1411.5	90.9	298	6	08SQH5	08sqh5 bos taurus
4	1377.5	88.7	298	13	09YIC4	09yic4 rana rugosa
5	1377.5	88.7	298	13	09PRH1	09prh1 rana rugosa
6	1374.5	88.5	298	13	09PRH2	09prh2 rana rugosa
7	1366.5	88.0	298	13	0919M9	0919m9 xenopus laevis
8	1245.5	80.2	299	5	095VX4	095vx4 ethmostigmus
9	1241.5	79.9	300	5	09NHV5	09nhv5 lucilia cup
10	1241.5	79.9	299	5	095S30	095s30 drosophila
11	1234.5	79.5	317	13	091336	091336 rana sylvatica
12	1183	76.2	288	5	044093	044093 drosophila
13	1183	76.2	288	5	044094	044094 drosophila
14	1147	73.9	307	5	062526	062526 drosophila
15	1139.5	73.4	304	5	025129	025129 halocynthia
16	1101.5	70.9	315	4	09HOC2	09hoc2 homo sapien

17	1045.5	67.3	313	5	P91410	P91410 caenorhabdi
18	1043.5	67.2	313	5	021103	021103 caenorhabdi
19	1037.5	66.8	300	5	045865	045865 caenorhabdi
20	1005.5	64.7	300	5	001813	001813 caenorhabdi
21	993.5	64.0	300	5	017407	017407 caenorhabdi
22	989.5	63.7	309	5	097470	097470 dictyostell
23	959	61.8	307	8	09XM22	09XM22 ascaris suu
24	950	61.2	318	5	09B136	09B136 toxoplasma
25	905.5	58.3	301	5	025692	025692 plasmodium
26	904.5	58.2	301	5	026006	026006 plasmodium
27	841.5	54.2	170	6	09XS69	09XS69 sus scrofa
28	772	49.7	306	5	018683	018683 caenorhabdi
29	757.5	48.8	305	3	09PM1	09PM1 yarrowia li
30	750.5	48.3	307	5	076286	076286 trypanosoma
31	746.5	48.2	303	3	074260	074260 candida par
32	746.5	48.1	379	10	049447	049447 arabidopsis
33	745.5	48.0	326	5	P91270	P91270 caenorhabdi
34	743.5	47.9	307	5	026697	026697 trypanosoma
35	740.5	47.7	386	10	P93767	P93767 lycopersico
36	738.5	47.6	388	10	049875	049875 lupinus alb
37	731.5	47.1	317	5	09N647	09N647 leishmania
38	728.5	46.9	306	3	P78754	P78754 schizosacch
39	727.5	46.8	331	10	041628	041628 triticum tu
40	708	45.6	305	3	09P876	09P876 pichia jadi
41	705	45.4	305	3	09P875	09P875 pichia jadi
42	698	44.9	308	3	08FEA7	08FEA7 neocallimas
43	681	43.9	330	10	09FM86	09FM86 arabidopsi
44	676	43.5	298	5	021809	021809 caenorhabdi
45	659	42.4	262	10	09AVT6	09AVT6 picea abies

ALIGNMENTS

RESULT 1

ID	046373	PRELIMINARY:	PRT:	298 AA.
AC	046373:			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	ADP/ATP translocase.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_Taxid=9986;			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RC	TISSUE=SKLETAL MUSCLE;			
RA	Yamauchi N., Kasai M.;			
RT	"Identification of a 30kDa calsequestrin-binding protein, which			
RT	regulates calcium release from sarcoplasmic reticulum of rabbit			
RT	skeletal muscle.";			
RL	J. Biochem. 335:541-547(1998).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL			
CC	INNER MEMBRANE (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
DR	EMBL: AB009386; BAA23777.1; -.			
DR	InterPro: IPR001993; Mitoch_carrier.			
DR	InterPro: IPR02067; Mit_carrier.			
DR	Pfam: PF00153; mto_carr; 3.			
DR	PRINTS: PR00926; MITOCARRIER.			
DR	PROSITE: PS00215; MITOCH_CARRIER; 3.			
KW	Inner membrane; Mitochondrion; Transmembrane; Transport.			
SO	SEQUENCE 298 AA; 32901 MW; CAEA32C8B164AD78 CRC64;			
QY	Query Match	94.3%:	Score 1464.5:	DB 6: Length 298;
	Best Local Similarity	94.6%:	Pred. No. 6.2e-126;	
	Matches 282; Conservative	7;	Mismatches 8;	Indels 1;
			Gaps 1;	
Db	1 MGDHMSFLKDFLAGAVAAVSKTAVAPIERVKLLLYQVHASKOISAKOYKGIIDCVVR 60			
	1 MSDQSLFKDFLAGVAAVSKTAVAPIERVKLLLYQVHASKOISAKOYKGIIDCVVR 60			

Oy	61	IPKEGFLSEFMNGNLANNIYRPEPTQALNPAFEDKTKKOLFEGVDHKKEMWRFAENGLASG	120
Dd	61	IPKEGFLSEFMNGNLANNIYRPEPTQALNPAFEDKTKKOLFEGVDHKKEMWRFAENGLASG	120
Oy	121	GAAGATSLCEVYPDLPDFARTRLAADVG-R-RAQRREFGLGPCILIKIRKSJDLRLGYGFNVS	179
Dd	121	GAAGATSLCEVYPDLPDFARTRLAADVGKAQAQREFGSLGNCLFKIRKSDGLRGLYGFNVS	180
Oy	180	VGGIIIVRAAYGVYDTAKGMLPDPKNHHIPIPSMMIAOSYTVAVAGLLSPFTVRRRAMM	239
Dd	181	VGGIIIVRAAFGVYDTAKGMLPDEKNHHIIVSMIAOTVTVAVALYSVPFTVRRRAMM	240
Oy	240	QSGRGADIMYTGTDCMKRIKADGCARAFKFGAMSNNVRGGAFFVLTYDEIRKYV	297
Dd	241	QSGRGADIMYTGTVCCKRKIKADGCARAFKFGAMSNNVRGGAFFVLTYDEIRKYV	298
 RESULT 2 062164 PRELIMINARY; PRT: 298 AA.			
ID	062164		
AC	062164		
DI	01-NOV-1996 (TREMBlrel. 01, Created)		
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)		
DR	01-JUN-2002 (TREMBlrel. 21, Last annotation update)		
DE	Adenine nucleotide carrier (adenine nucleotide translocase 1) (Similar to solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4) (Hypothetical 32.9 kDa protein).		
GN	SLOC25A4 OR MANC1 OR ANTL.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C; TISSUE=MUSCLE;		
RA	Laplace C., Costet P.;		
RL	Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Ley S.E., Chen Y.-S., Graham B.H., Wallace D.C.;		
RT	"Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes."		
RL	Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Straussberg R.;		
RL	Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=EYE;		
RA	Straussberg R.;		
RL	Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.		
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL		
CC	-I- INNER MEMBRANE (BY SIMILARITY).		
CC	-I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.		
DR	EMBL: X74510; CAAS2616.1; -		
DR	EMBL: AF240002; AAF64470.1; -		
DR	EMBL: BC003791; AAH03791.1; -		
DR	EMBL: BC026925; AAH26925.1; -		
DR	MGI: MGI:1353495; Slc25a4.		
DR	InterPro: IPR001993; Mitoch_carrier.		
DR	InterPro: IPR002067; Mit_carrier.		
DR	Pfam: PF00153; mito_carr_3.		
DR	PRINTS: PR00926; MITOCARRIER.		
DR	PROSITE: PS00215; MITOCH_CARRIER; 3.		
KW	Hypothetical protein; Inner membrane; Repeat; Transmembrane; Transport; Mitochondrion.		
SO	SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CNC64;		
 Query Match 94.2%; Score 1463.5; DB 11; Length 298; Best Local Similarity 94.0%; Pred. No. 7.7e-126; Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;			

ID	Q9YIC4	PRELIMINARY:	PRT:	298 AA.
QY	1	MCDHMSFLKDPDLACGAAVAASKTAVAPLERKLLLOVHASKOISAEQYGIIDCYVR	60	
Db	1	MCDQALSLFKDPLAGGIAAASKTAAAPLERKLLLOVHASKOISAEQYGIIDCYVR	60	
QY	61	IKKEGGLSLFWMKGNLANVIRYFTQALNFAFDKTKYKQLFLGVDNRHKQFWRFFAGNLASG	120	
Db	61	IKKEGGLSLFWMKGNLANVIRYFTQALNFAFDKTKYKQLFLGVDNRHKQFWRFFAGNLASG	120	
QY	121	GAGATSLCFVYPLDFAPTRLADYGR-RAQREPHGLDGCITIKRSDGLRGLYOGFNVS	179	
Db	121	GAGATSLCFVYPLDFAPTRLADYGR-RAQREPHGLDGCITIKRSDGLRGLYOGFNVS	180	
QY	180	VGGIITIRAAHYGVYDTAGKMLPDPKNNHIFPSMMIAQSVTAAGLSTYPTPTVRRRMM	239	
Db	181	VGGIITIRAAHYGVYDTAGKMLPDPKNNHIFPSMMIAQSVTAAGLSTYPTPTVRRRMM	240	
QY	240	QSGRGADIMYGTVDCKWKIAKDEGAKAFFGAGSNVLRGNGAGFVLYLDEIKKY	296	
Db	241	QSGRGADIMYGTVDCKWKIAKDEGAKAFFGAGSNVLRGNGAGFVLYLDEIKKY	297	
RESULT 4				
ID	Q9YIC4	PRELIMINARY:	PRT:	298 AA.
QY	1	MCDHMSFLKDPDLACGAAVAASKTAVAPLERKLLLOVHASKOISAEQYGIIDCYVR	60	
Db	1	MCDQALSLFKDPLAGGIAAASKTAAAPLERKLLLOVHASKOISAEQYGIIDCYVR	60	
QY	61	IKKEGGLSLFWMKGNLANVIRYFTQALNFAFDKTKYKQLFLGVDNRHKQFWRFFAGNLASG	120	
Db	61	IKKEGGLSLFWMKGNLANVIRYFTQALNFAFDKTKYKQLFLGVDNRHKQFWRFFAGNLASG	120	
QY	121	GAGATSLCFVYPLDFAPTRLADYGR-RAQREPHGLDGCITIKRSDGLRGLYOGFNVS	179	
Db	121	GAGATSLCFVYPLDFAPTRLADYGR-RAQREPHGLDGCITIKRSDGLRGLYOGFNVS	180	
QY	180	VGGIITIRAAHYGVYDTAGKMLPDPKNNHIFPSMMIAQSVTAAGLSTYPTPTVRRRMM	239	
Db	181	VGGIITIRAAHYGVYDTAGKMLPDPKNNHIFPSMMIAQSVTAAGLSTYPTPTVRRRMM	240	
QY	240	QSGRGADIMYGTVDCKWKIAKDEGAKAFFGAGSNVLRGNGAGFVLYLDEIKKY	296	
Db	241	QSGRGADIMYGTVDCKWKIAKDEGAKAFFGAGSNVLRGNGAGFVLYLDEIKKY	297	

```
AC 09YIC4:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (wrinkled frog).
OC Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT 2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC INNER MEMBRANE (BY SIMILARITY).
DR EMBL; AB008457; BAA36507.1; -
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr. 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B370ED37099A00 CRC64;

Query Match 88.7%; Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%; Pred. No. 5,7e-118;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGHANSELDPLAGAAVAAVSKTAVAPIERVKLLLOVQASHKOISAEKQYKGIIDCVVR 60
DB 1 MTDALISFADFLAGVAAAIKSTAVAPIERVKLLLOVQASHKOITADKQYKGIIDCVVR 60
OY 61 IPKEQGFSEFWRGMLNAVIRFPTQALNFAFKDKYKQLFLGVDRHKKQFRRYFAGNLASG 120
DB 61 IPKEQGFSEFWRGMLNAVIRFPTQALNFAFKDKYKQLFLGVDRHKKQFRRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVGRGRR-AQREFHGLDCTIKFKSDGLKGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGRGRR-AQREFHGLDCTIKFKSDGLKGLYOGFNVS 180
OY 180 VQGIITIRAAVFGYVDPAKGLPDPKRVHIFVSMINQSTAVAGLLSYFEDTVRRRMM 239
DB 180 VQGIITIRAAVFGYVDPAKGLPDPKRVHIFVSMINQSTAVAGLLSYFEDTVRRRMM 240
OY 240 QSGRKAGADIVYTGVDCKRKRIAKDEGAKAFKFGAMSVNLKMGCAFVLVLYDEIKKYV 297
DB 241 QSGRKAGADIVYTGVDCKRKRIAKDEGAKAFKFGAMSVNLKMGCAFVLVLYDEIKKYI 298

RESULT 5
O9PRH1 PRELIMINARY; PRT; 298 AA.
AC 09PRH1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (wrinkled frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
```

```
RT 2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC INNER MEMBRANE (BY SIMILARITY).
DR EMBL; AB008463; BAA36513.1; -
DR EMBL; AB008456; BAA36506.1; -
DR EMBL; AB008461; BAA36511.1; -
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr. 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 88.7%; Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%; Pred. No. 5,7e-118;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGHANSELDPLAGAAVAAVSKTAVAPIERVKLLLOVQASHKOISAEKQYKGIIDCVVR 60
DB 1 MTDALISFADFLAGVAAAIKSTAVAPIERVKLLLOVQASHKOITADKQYKGIIDCVVR 60
OY 61 IPKEQGFSEFWRGMLNAVIRFPTQALNFAFKDKYKQLFLGVDRHKKQFRRYFAGNLASG 120
DB 61 IPKEQGFSEFWRGMLNAVIRFPTQALNFAFKDKYKQLFLGVDRHKKQFRRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVGRGRR-AQREFHGLDCTIKFKSDGLKGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGRGRR-AQREFHGLDCTIKFKSDGLKGLYOGFNVS 180
OY 180 VQGIITIRAAVFGYVDPAKGLPDPKRVHIFVSMINQSTAVAGLLSYFEDTVRRRMM 239
DB 180 VQGIITIRAAVFGYVDPAKGLPDPKRVHIFVSMINQSTAVAGLLSYFEDTVRRRMM 240
OY 240 QSGRKAGADIVYTGVDCKRKRIAKDEGAKAFKFGAMSVNLKMGCAFVLVLYDEIKKYV 297
DB 241 QSGRKAGADIVYTGVDCKRKRIAKDEGAKAFKFGAMSVNLKMGCAFVLVLYDEIKKYI 298

RESULT 6
O9PRH2 PRELIMINARY; PRT; 298 AA.
AC 09PRH2:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (wrinkled frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT 2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC INNER MEMBRANE (BY SIMILARITY).
DR EMBL; AB008460; BAA36510.1; -
DR EMBL; AB008458; BAA36508.1; -
DR EMBL; AB008459; BAA36509.1; -
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
```

DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 88.5%; Score 1374.5; DB 13; Length 298;
 Best Local Similarity 86.2%; Pred. No. 1,le-117;
 Matches 257; Conservative 24; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKFLAGVAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
 DB 1 MTDALISPAKDFLAGVAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
 QY 61 IPKGGFLSPWGRNLANYIRFPFOALNFARFKDKYKQFLGVDGRHGFWRFPAGNLSG 120
 DB 61 IPKGGFLSPWGRNLANYIRFPFOALNFARFKDKYKQFLGVDGRHGFWRFPAGNLSG 120
 QY 121 GAAGATSLCFEYPLDFARTRLADYGR-AQREFHGLGDCIIRKSPDGLRGLYOGFNV 179
 DB 121 GAAGATSLCFEYPLDFARTRLADYGR-AQREFHGLGDCIIRKSPDGLRGLYOGFNV 180
 QY 180 VGGIITRAAFYGYDTAKGMLPDPKKNVHIFVSMIAQSVTAAGLSYPPDYVRRMM 239
 DB 181 VGGIITRAAFYGYDTAKGMLPDPKKNVHIFVSMIAQSVTAAGLSYPPDYVRRMM 240
 QY 240 QSGRKGADIMTGVDCRKTAKDEGAKAFKGAAMSNVLRMGAFVLYLDEIKKYV 297
 DB 241 QSGRKGADIMTGVDCRKTAKDEGAKAFKGAAMSNVLRMGAFVLYLDEIKKYI 298

RESULT 7

Q919M9 PRELIMINARY: PRT: 298 AA.

AC Q919M9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Adenine nucleotide translocase.
 GN ANTL.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Livsage R.A.;
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
 RT Dynamic Patterns of Expression During Development."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF31347; AAF63471.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 88.0%; Score 1366.5; DB 13; Length 298;
 Best Local Similarity 86.2%; Pred. No. 5,8e-117;
 Matches 257; Conservative 23; Mismatches 17; Indels 1; Gaps 1;
 QY 1 MGDHMSFLKFLAGVAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
 DB 1 MTDALISPAKDFLAGVAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60

DB 1 MTDALISPAKDFLAGVAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 60
 QY 61 IPKGGFLSPWGRNLANYIRFPFOALNFARFKDKYKQFLGVDGRHGFWRFPAGNLSG 120
 DB 61 IPKGGFLSPWGRNLANYIRFPFOALNFARFKDKYKQFLGVDGRHGFWRFPAGNLSG 120
 QY 121 GAAGATSLCFEYPLDFARTRLADYGR-AQREFHGLGDCIIRKSPDGLRGLYOGFNV 179
 DB 121 GAAGATSLCFEYPLDFARTRLADYGR-AQREFHGLGDCIIRKSPDGLRGLYOGFNV 180
 QY 180 VGGIITRAAFYGYDTAKGMLPDPKKNVHIFVSMIAQSVTAAGLSYPPDYVRRMM 239
 DB 181 VGGIITRAAFYGYDTAKGMLPDPKKNVHIFVSMIAQSVTAAGLSYPPDYVRRMM 240
 QY 240 QSGRKGADIMTGVDCRKTAKDEGAKAFKGAAMSNVLRMGAFVLYLDEIKKYV 297
 DB 241 QSGRKGADIMTGVDCRKTAKDEGAKAFKGAAMSNVLRMGAFVLYLDEIKKYI 298

RESULT 8

Q95VX4 PRELIMINARY: PRT: 299 AA.

AC Q95VX4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP-ATP translocator.
 OS Ethmostigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
 OX NCBI_TaxID=62613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burnell J.N.;
 RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
 RT rubripes."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF401758; AAL02100.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN.2.
 SQ SEQUENCE 299 AA; 33037 MW; 3C3BBCB96E7C3C5E CRC64;

Query Match 80.2%; Score 1245.5; DB 5; Length 299;
 Best Local Similarity 80.3%; Pred. No. 7e-106;
 Matches 236; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

QY 5 AWSFLKDFLAGVAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 64
 DB 5 AVSFLKDFIAGVAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVR 64
 QY 65 QGFLSPWGRNLANYIRFPFOALNFARFKDKYKQFLGVDGRHGFWRFPAGNLSG 124
 DB 65 QGFLSPWGRNLANYIRFPFOALNFARFKDKYKQFLGVDGRHGFWRFPAGNLSG 124
 QY 125 ATSLCFEYPLDFARTRLADYGR-AQREFHGLGDCIIRKSPDGLRGLYOGFNV 183
 DB 125 ATSLCFEYPLDFARTRLADYGR-AQREFHGLGDCIIRKSPDGLRGLYOGFNV 184
 QY 184 IYRAAFYGYDTAKGMLPDPKKNVHIFVSMIAQSVTAAGLSYPPDYVRRMM 243
 DB 185 IYRAAFYGYDTAKGMLPDPKKNVHIFVSMIAQSVTAAGLSYPPDYVRRMM 244
 QY 244 KGADIMTGVDCRKTAKDEGAKAFKGAAMSNVLRMGAFVLYLDEIKKYV 297
 DB 245 KKADILYNTIDCWGKIYKTEGGAFFKGAAPSNILRGTGGAFFVLYLDEIKALI 298

RESULT 9

Q9NHM5 PRELIMINARY: PRT: 300 AA.

AC Q9NHM5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)

RN	[2]	SEQUENCE FROM N.A.
RP		STRAIN-BERKELEY;
RC		Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
RA		Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA		Girarde R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA		Miranda A., Mungall C.J., Nunoo J., Paeckel J., Paragas V., Park S.,
RA		Patel S., Phouaneavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA		Celniker S.;
RL		Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR		EMBL: AY060978; AAL28526.1; -
DR		EMBL: AY070894; AAL48516.1; -
DR		FlyBase; FBgn0003360; seSB.
DR		InterPro; IPR001993; Mitoch_carrier.
DR		Pfam; PF00153; mito_carri_3.
DR		PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_3.
SR		SEQUENCE 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;
SO		
<hr/>		
Qy	5	AWSFLKDFLAGVAAVAASKTAVAPERYKLLLYOVHASKOSIAEKORYGIDCVYRIKPE 64
Dd	7	AVGEFKDPLAGGISAAVSKTAVAPERKLLLYOVHISKIÖSPDKQGMWDCFRIPKE 66
Qy	65	QGFLSFMEGNLANVRYEPPTOLANFEAFDYKKQLFLGVSDRHKOFRFFAGNLASGAAG 124
Dd	67	QGFSEFMNGNLNAVIRYEPPTOLANFAFDKYKQVFGLGVDNKTPWRFFAGNLASGAAG 126
Qy	125	ATSLCFVYPDLDPARTRLADYGRRAQRFPHGLDCTIIKFPSDGIRGLYGPNWSVGIT 184
Dd	127	ATSLCFVYPDLDFARTRLDADTGKGQREFETGIGNLTIFKSDGIVGLYRGFGVSGVGI 186
Qy	185	IYRAYEFGVYDTAKMLDDPKNVHIEFVSMILAOASTVANAGLSYFPEDVRRRMMSQGR 244
Dd	187	IYRAYEFSPYDPAKMLDDPKNTPIYISMALAQVVTAAGLVSTPDTVRRRMMSQGR 246
Qy	245	GADIAYTGTVDVCRKIARDGAKAFFGKAWSNVLRGMGAFVLVYDEIKK 295
Dd	247	ATEVIYKMTLHCWATIANKQEGTGAFFKAFSNI LRGTGAFVLVYDEIKK 297
<hr/>		
RESULT 11		
ID	Q91336	PRELIMINARY; prt; 317 aa.
AC	Q91336:	
DT	01-NOV-1996	(TREMBLrel. 01, Created)
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)
DE	ADP/ATP translocase.	
OS	Rana sylvatica (wood frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.	
OX	NCBI_TaxID=45438;	
RN	[1]	
RP		SEQUENCE FROM N.A.
RC		TISSUE-LIVER:
RX		MEDLINE=97398141; PubMed=9256066;
RA		Cal O., Greenway S.C., Storey K.B.;
RT		"Differential regulation of the mitochondrial ADP/ATP translocase gene
RL		in wood frogs under freezing stress.";
RN		Biochim. Biophys. Acta 1353:69-78(1997).
<hr/>		
RE		SEQUENCE FROM N.A.
RC		TISSUE-LIVER:
RA		Cal O., Storey K.B.;
RL		Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
CC	-1-	SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC	-1-	INNER MEMBRANE (BY SIMILARITY).
CC	-1-	SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR	EMBL; U44832; AAA97882.2; -	
DR	InterPro; IPR001993; Mitoch_carrier.	

DR InterPro: IPR002067; Mito_carrier.
 DR Pfam: PF00153; mito_carrier.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transport.
 SO SEQUENCE 317 AA; 35005 MW; 5f66b7e8dbd5ceb72 cnc64.

Query Match 79.5%; Score 1234.5; DB 13; Length 317;
 Best Local Similarity 85.7%; Pred. No. 7.6e-105;
 Matches 233; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

OY 1 MODHMSFLKDFLAGVAAVASTAVAPIERKLLLOVQHASKQISAEKQYGIIDCVYR 60
 DB 1 MTDANMSFAKDFLAGVAAVASTAVAPIERKLLLOVQHASKQITAKQYGIIDCVYR 60
 OY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFKDKYQVFLGVDRHKKOFWRFAGNLASG 120
 DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFKDKYKIFLDVNDKRTQFWRFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADYGR-AOREFHGLDCIIRKISDGLRGLYGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADYGRAGAGREFNGDLCKIRKISDGLRGLYGFNV 180
 OY 180 VQGIITVRAAYRGVDTAKGMLPDKNVHIFVSMIAQSVTAAGLSYPTVRRMM 239
 DB 181 VQGIITVRAAYRGVDTAKGMLPDKNVHIFVSMIAQSVTAAGLSYPTVRRMM 240
 OY 240 QSGRKADIMYTGVDCKRIKADGAKAFK 271
 DB 241 QSGRKAEIMYSGTIDCKRIKADGGRAFR 272

RESULT 12
 O44093 PRELIMINARY; PRT; 288 AA.
 ID 044093:
 AC 044093:
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila pseudoobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DB EMBL: AF025798; AAB87883.1; -
 DB FlyBase: FBgn0023292; dpseVesB.
 DR InterPro: IPR001993; MitoCh_carrier.
 DR Pfam: PF00153; mito_carrier; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 FT SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
 Best Local Similarity 79.6%; Pred. No. 3.5e-100;
 Matches 226; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

OY 5 AMSFLKDLAGVAAVASTAVAPIERKLLLOVQHASKQISAEKQYGIIDCVYR 64
 DB 7 AIGFVKDFAAGGISAASVSTAVAPIERKLLLOVQHASKQISPDQYGMVDCFRIRKE 66
 OY 65 QGFLSFWGNLANVIRYPTQALNFAFKDKYQVFLGVDRHKKOFWRFAGNLASG 124

DB 67 QGFLSFWGNLANVIRYPTQALNFAFKDKYQVFLGVDRHKKOFWRFAGNLASG 126
 OY 125 ATSLCFVYPLDFARTRLADYGRRAOREFHGLDCIIRKISDGLRGLYGFNV 184
 DB 127 ATSLCFVYPLDFARTRLADYGRRAOREFHGLDCIIRKISDGLRGLYGFNV 186
 OY 185 IYRAVFGVDTAKGMLPDKNVHIFVSMIAQSVTAAGLSYPTVRRMMQSGRK 244
 DB 187 IYRAVFGVDTAKGMLPDKNVHIFVSMIAQSVTAAGLSYPTVRRMMQSGRK 245
 OY 245 GADIMYTGVDCKRIKADGAKAFKAGMSVLRGKGAFLV 288
 DB 246 ATEIITKNTLHGMATIAKQEG-AFFKGAFAFNVLRGTGAFV 288

RESULT 13
 O44094 PRELIMINARY; PRT; 288 AA.
 ID 044094:
 AC 044094:
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila subobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DB EMBL: AF025799; AAB87884.1; -
 DB FlyBase: FBgn0023237; DsubVesB.
 DR InterPro: IPR001993; MitoCh_carrier.
 DR Pfam: PF00153; mito_carrier; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 FT SEQUENCE 288 AA; 31775 MW; 06A1D1E477B81B26 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
 Best Local Similarity 79.6%; Pred. No. 3.5e-100;
 Matches 226; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

OY 5 AMSFLKDLAGVAAVASTAVAPIERKLLLOVQHASKQISAEKQYGIIDCVYR 64
 DB 7 AMGFVKDFAAGGISAASVSTAVAPIERKLLLOVQHASKQISPDQYGMVDCFRIRKE 66
 OY 65 QGFLSFWGNLANVIRYPTQALNFAFKDKYQVFLGVDRHKKOFWRFAGNLASG 124
 DB 67 QGFLSFWGNLANVIRYPTQALNFAFKDKYQVFLGVDRHKKOFWRFAGNLASG 126
 OY 125 ATSLCFVYPLDFARTRLADYGRRAOREFHGLDCIIRKISDGLRGLYGFNV 184
 DB 127 ATSLCFVYPLDFARTRLADYGRRAOREFHGLDCIIRKISDGLRGLYGFNV 186
 OY 185 IYRAVFGVDTAKGMLPDKNVHIFVSMIAQSVTAAGLSYPTVRRMMQSGRK 244
 DB 187 IYRAVFGVDTAKGMLPDKNVHIFVSMIAQSVTAAGLSYPTVRRMMQSGRK 245
 OY 245 GADIMYTGVDCKRIKADGAKAFKAGMSVLRGKGAFLV 288
 DB 246 ATEIITKNTLHGMATIAKQEG-AFFKGAFAFNVLRGTGAFV 288

RESULT	14			
ID	062526	PRELIMINARY;	PRT:	307 AA.
AC	062526			
DT	01-AUG-1998 (TREMBLrel. 07, Created)			
DR	01-AUG-1998 (TREMBLrel. 07, Last sequence update)			
DE	01-JUN-2001 (TREMBLrel. 17, last annotation update)			
GN	ANT2 protein.			
OS	ANT2 OR CG1683.			
OC	Drosophila melanogaster (Fruit fly).			
CC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
CC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
CC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBTaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BERKELEY.			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Richards S.E., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers J.-H.C., Blazer R.G., Chame M., Pfeiffer B.D., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D., Baller R.M., Basu A., Baxendale J., Bayraktaroglu T., Beasley E.M., Beeson K.Y., Benos P.V., Bereman B.P., Bhargava D., Bolshakov S., Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P., Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Duan A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Gloddek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kittel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z., Luo X.P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Meknoul G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Munzy D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paciel J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Putl V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirydas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yah R.-F., Zavari J.S., Zhao M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;			
RT	The genome sequence of Drosophila melanogaster."			
RL	Science 287:2185-2195(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-OREGON-R.			
RA	Zhang Y.Q., Davis A.W., Roote J., Ashburner M., Submitted (May-1998) to the EMBL/Genbank/DBD databases.			
RL	EMBL; AE003484; AA047956.1; -			
DR	EMBL; Y10618; CAAT1629.1; -			
DR	FlyBase; FBgn002511; Ant2.			
DR	InterPro; IPRO01993; Mitoch_carrier.			
DR	InterPro; IPRO02067; Mit_carrt.			
DR	Pfam; PF00153; mito_carr_3.			
DR	PRINTS; PR00926; MITOCARRIER.			
DR	PROSITE; PS00215; MITOC_CARRIER; UNKNOWN_2.			
SO	SEQUENCE 307 AA; 33744 MW; 3D6B3DFD82061C CRC64;			

	Matches	214:	Conservative	33:	Mismatches	43:	Indels	0:	Gaps	0:
QY	7	SFLKDFLAGAANAASKA	TA	VARIPIREVKLLLOV	HASKOISAEKYKGIIDCVVRIPKEOG	66				
Db	17	SFLMDFMGGSVAIAAKTAP	IAPIERVKLLILOVESSKOIAAOQRKGIVDCFRIRPKEOG	76						
QY	67	FLSPFGRGLANVIATREPTQALNFAFKDKDYKOLFSGVDPRHROFWMYRFGNLASGGAAAGT	126							
Db	77	FSSFEWRGNLANVIATREPTQALNFAFKDKDYKSYSLGVDYHKOFWHRFAGNLASGGAAAGT	136							
QY	127	SLCEFYPPDFAFTRILAAAVGRRAROREPFIIGLGCIIKIFKSDRLRGLYOGFNYSVOGIITY	186							
Db	137	SLCFEYPLDPARTRIADAVGCKGRNEFPNLDCLMKVIKSDPITGLRFETIYSVGIVTY	196							
QY	187	RAAFGVYDTAKGMLPDRKNHIIFYSWMIADSVTAVALLSYPDPTRRRMMOSGRKA	246							
Db	197	RAAFGEYDFCRDEPLPNRPKSTPFPEYSMAIQAQVTTVAGIASYFPDTRRRMMOSGLKKS	256							
QY	247	DIMTGTYDCMRKIATKDEGAKEFFEGANSNVLRGGAGFVLVLYDEIKRY	296							
Db	257	EMVYNKNTACMLVIAKOGSIGAFFEGALSNIIRGTGALVIALYLAIDEMKKY	306							
RESULT	15									
ID	025129	PRELIMITARY;	PRT:	304	AA.					
AC	025129;									
DT	01-NOV-1996	(TREMBLrel. 01, Created)								
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)								
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)								
DE	ADP/ATP translocase.									
GN	HRATL1.									
OS	Halocynthia roretzi (Sea squirt).									
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;									
OC	Stolidobranchia; Pyuridae; Halocynthia.									
OX	NCBI_TaxID=7729;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RA	Mya T.;									
RL	submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.									
RN	[2]									
RP	SEQUENCE FROM N.A.									
RA	Mya T., Makabe K., Satoh N.;									
RT	"Expression of a gene for major mitochondrial protein, ADP/ATP translocase, during embryogenesis in the ascidian Halocynthia roretzi.";									
RT	Dev. Growth Differ. 36:39-48(1994).									
RL	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (By SIMILARITY).									
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.									
DR	EMBL; D83069; BAAL1765.1;"									
DR	InterPro; IPR001993; Mitoch_carrler.									
DR	InterPro; IPR002067; Mlt_carrier.									
DR	Pfam; PF00153; mto_carrt_3									
DR	PRINTS; PR00926; MITOCARRIER.									
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.									
KW	Inner membrane; Mitochondrion; Transmembrane; Transport.									
SO	SEQUENCE 304 AA; 33307 MW; 51FD0D7DEB654880 CRC64;									
Query Match		73.4%;	Score 1139.5;	DB 5;	Length 304;					
Best Local Similarity		74.6%;	Freq. No. 3.6e-96;							
Matches	220:	Conservative	18:	Mismatches	54:	Indels	3:	Gaps	1:	
QY	6	WS---FLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISA	EOKYGIIDCVVRIP	62						
Db	3	WSANDFAFDLAIIGCAAAIAISTKIYAPIERVKLLLOVAVSTOMKAGTEKGIITDAFVRIP	62							
QY	63	KEQGLFSWRGNLANVIATREPTQALNFAEFKDYKOLFSGVDPRHROFWMYRFGNLASGA	122							
Db	63	KEQGFFSLMGRNLAVIATREPTQALNFAFKDYTKRIFLAGVDKRQGFMYRFGNLASGA	122							
QY	123	AGATSLSGVYPLDPARTRIADAVGRRAROREPFIIGLDCIIKIFKSDRLRGLYOGFNYSVOG	182							

Db 123 AGATGCTCTVPLDPAFTRRLAADIGSGGSRQFTGLGNCIATIVKKDGPRLYQGFVVSIOG 182
QY 183 IIVRAAFEGYDTAKGMLPDPKNVHIFVSMIAOSYTAVALSLSPEDTVRRMMOSG 242
Db 183 IIVRAAFEGYDTAKGMLPDPKNVHIFVSMIAOSYTAVALSLSPEDTVRRMMOSG 242
QY 243 RKGADIMTGTVDGWRKTADEGAKAFKAGMSNVLRGMSAFVLYDEIKKY 297
Db 243 RKGADIMTGTVDGWRKTADEGAKAFKAGMSNVLRGMSAFVLYDEIKKY 297

Search completed: November 12, 2002, 16:47:49
Job time : 27.2766 secs

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX
XX WPI: 2000-365619/31.
DR N-PSDB: AAD00520.
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
PS Claim 45; Page 172-173; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT2 from human brain.
XX
SQ Sequence 298 AA:

Query Match 100.0%; Score 1547; DB 21; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-154;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSFKDPDLGAGVAAIAISKTAVAPIERVKLLQOVHASKQITADQYGIIDCVR 60
DB 1 MTDALSFKDPDLGAGVAAIAISKTAVAPIERVKLLQOVHASKQITADQYGIIDCVR 60
QY 61 IRKDEEVLSEFMGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQWRFPAGLASG 120
DB 61 IRKDEEVLSEFMGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQWRFPAGLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGCLVKIKYSDIKGLYGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGCLVKIKYSDIKGLYGFNVS 180
QY 181 VGGIITIRAAFGIYDTAKGMLPDPKNTIIVISWMAIQVTVAVAGLTSYPPDTRRRMM 240
DB 181 VGGIITIRAAFGIYDTAKGMLPDPKNTIIVISWMAIQVTVAVAGLTSYPPDTRRRMM 240
QY 241 QSGRKGTDMYGTLDPCWKRIARDEGKAFKFGAMSNTLRGMGAFVLYLDEIKKYYT 298
DB 241 QSGRKGTDMYGTLDPCWKRIARDEGKAFKFGAMSNTLRGMGAFVLYLDEIKKYYT 298

RESULT 2
AAU01199
ID AAU01199 standard; Protein; 298 AA.
AC
XX AAU01199;
XX
XX 07-SEP-2001 (first entry)
DE Human adenine nucleotide translocator-2 (ANT-2) protein.
XX
XX Human adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX

OS Homo sapiens.
XX
XX WO200132876-A2.
XX
XX 10-MAY-2001.
XX
XX 03-NOV-2000; 2000MO-US30535.
XX
XX 03-NOV-1999; 99US-0434354.
XX
XX (MITO-) MITOKOR.
XX
XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Figeri LG;
PI Velicelebi G, Davis RE;
XX
XX WPI: 2001-291054/30.
DR N-PSDB: AAS05902.
XX
XX New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
PS Disclosure; Fig 2: 186pp; English.
XX
XX The present sequence represents human adenine nucleotide translocator-2
CC (ANT-2) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ Sequence 298 AA:

Query Match 100.0%; Score 1547; DB 22; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-154;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSFKDPDLGAGVAAIAISKTAVAPIERVKLLQOVHASKQITADQYGIIDCVR 60
DB 1 MTDALSFKDPDLGAGVAAIAISKTAVAPIERVKLLQOVHASKQITADQYGIIDCVR 60
QY 61 IRKDEEVLSEFMGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQWRFPAGLASG 120
DB 61 IRKDEEVLSEFMGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQWRFPAGLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGCLVKIKYSDIKGLYGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGCLVKIKYSDIKGLYGFNVS 180
QY 181 VGGIITIRAAFGIYDTAKGMLPDPKNTIIVISWMAIQVTVAVAGLTSYPPDTRRRMM 240
DB 181 VGGIITIRAAFGIYDTAKGMLPDPKNTIIVISWMAIQVTVAVAGLTSYPPDTRRRMM 240
QY 241 QSGRKGTDMYGTLDPCWKRIARDEGKAFKFGAMSNTLRGMGAFVLYLDEIKKYYT 298
DB 241 QSGRKGTDMYGTLDPCWKRIARDEGKAFKFGAMSNTLRGMGAFVLYLDEIKKYYT 298

RESULT 3

AAU10379
 ID AAU10379 standard; Protein: 298 AA.
 AC AAU10379;
 DT 14-FEB-2002 (first entry)
 XX
 DE Human adenine nucleotide translocator 2 (ANT2).
 XX
 KM Human: adenine nucleotide translocator; ANT; ss;
 KM mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200165944-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 11-MAY-2001; 2001WO-US15416.
 XX
 PR 11-MAY-2000; 2000US-0569327.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
 DR WPI: 2002-055598/07.
 DR N-PSDB; AAS16689.
 XX
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 XX
 PS Claim 44; Fig 2; 147pp; English.
 XX
 CC The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT2.
 CC
 XX
 SQ Sequence 298 AA:
 Query Match 100.0%; Score 1547; DB 23; Length 298;
 Best Local Similarity 100.0%; Pred. 2.5e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MTDALSPFKKDFLAGVAAAIKSTAVAPTEIRVLLQVOHASKQITADKQYKGIIDCVYR 60
 DB 1 MTDALSPFKKDFLAGVAAAIKSTAVAPTEIRVLLQVOHASKQITADKQYKGIIDCVYR 60
 OY 61 IPKEQEVLSFWRGNTLVNIRYPTQALNFAFKDKYKQIFLGVDKRTQEFNRYFAGNLASG 120
 DB 61 IPKEQEVLSFWRGNTLVNIRYPTQALNFAFKDKYKQIFLGVDKRTQEFNRYFAGNLASG 120
 OY 121 GAAGATSLCEFYVPLDFAKRLADVGKAGAREFRGLGCTLVKTIYSDGKIGKYGQFNVS 180
 DB 121 GAAGATSLCEFYVPLDFAKRLADVGKAGAREFRGLGCTLVKTIYSDGKIGKYGQFNVS 180
 OY 181 VGGIITRYRAAYFGIYDTAKGMLPDPKNTHTIVISMTAQFTVAVAGLTSTYPTDVRRRMM 240

DB 181 VGGIITRYRAAYFGIYDTAKGMLPDPKNTHTIVISMTAQFTVAVAGLTSTYPTDVRRRMM 240
 OY 241 QSGRKGTDMWYGTGLDCWRKRIARDEGKAFKGCAMSVNLKGMGAPVLVYDEIKKYYT 298
 DB 241 QSGRKGTDMWYGTGLDCWRKRIARDEGKAFKGCAMSVNLKGMGAPVLVYDEIKKYYT 298
 RESULT 4
 ID AAU71033 standard; Protein: 298 AA.
 AC AAU71033;
 DT 29-AUG-2000 (first entry)
 XX
 DE Human adenine nucleotide translocator ANT3.
 XX
 KM Human: adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
 KM adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KM mitochondrial permeability transition; neuroprotective; neotrophic;
 KM antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KM antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KM diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KM mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KM mitochondrial diabetes and deafness; hyperproliferative disorder;
 KM myoclonic epilepsy red ragged fibre syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200026370-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 03-NOV-1999; 99WO-US25883.
 XX
 PR 03-NOV-1998; 98US-0185904.
 XX
 PR 08-SEP-1999; 99US-0393441.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS;
 DR WPI: 2000-365619/31.
 DR N-PSDB; AAD00521.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 46; Page 173-174; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 CC
 XX
 SQ Sequence 298 AA:

Query Match	94.0%	Score 1454	DB 21	Length 298
Best Local Similarity	92.6%	Pred. No. 1.5e-144		
Matches 274	Conservative 13	Mismatches 9	Indels 0	Gaps 0
QY	1	MTPALISFADFLAGGVAALISKTAAPLIERVKLLQOVHASKQLTADKQYKGIIDCVVR	60	
Db	1	MTQDAISFADFLAGGVAALISKTAAPLIERVKLLQOVHASKQLTADKQYKGIIDCVVR	60	
QY	61	IPKQEVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRPQFWRYFAGNLASG	120	
Db	61	IPKQEVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRPQFWRYFAGNLASG	120	
QY	121	GAGATSLCQVYLPDFAKRLADVCKAGAREFERGIGCIQVITYSDSGIKGIYQGFNVS	180	
Db	121	GAGATSLCQVYLPDFAKRLADVCKAGAREFERGIGCIQVITYSDSGIKGIYQGFNVS	180	
QY	181	VQGIITRAYAFEGIYDPAKGMLEDPKNTHTIVISMIAQVTAAGLTSYFPDTRRRMM	240	
Db	181	VQGIITRAYAFEGIYDPAKGMLEDPKNTHTIVISMIAQVTAAGLTSYFPDTRRRMM	240	
QY	241	QSGRKGTDIWYTGTLDCWKRILANDEGKAFFKGAMSNVLRGMGAFVLYLDEIKR	296	
Db	241	QSGRKGTDIWYTGTLDCWKRILANDEGKAFFKGAMSNVLRGMGAFVLYLDEIKR	296	
RESULT 5				
AAM39641	ID	AAM39641 standard; Protein: 298 AA.		
XX		AAM39641;		
XX	DT	22-OCT-2001 (first entry)		
XX		Human polypeptide SEQ ID NO 2786.		
XX		Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;		
KM		peripheral nervous system; neuropathy; central nervous system; CNS;		
KM		Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
KM		amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;		
KW		chemokine; thrombolytic; drug screening; arthritis; inflammation;		
KW		Leukaemia.		
OS		Homo sapiens.		
XX				
XX		MO200153312-AL.		
XX				
XX	PD	26-JUL-2001.		
XX				
XX	PF	26-DEC-2000; 2000MO-US34263.		
XX				
XX	21-JAN-2000;	2000US-0488725.		
PR	25-APR-2000;	2000US-0552317.		
PR	09-JUL-2000;	2000US-0598042.		
PR	19-JUL-2000;	2000US-0620312.		
PR	03-AUG-2000;	2000US-0653450.		
PR	14-SEP-2000;	2000US-0662191.		
PR	19-OCT-2000;	2000US-0693036.		
PR	29-NOV-2000;	2000US-0727344.		
XX				
XX		(HYSE-) HYSEQ INC.		
XX				
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;			
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;			
PI	Zhao QA, Zhou P, Goodrich R, Dirmnac RT;			
XX				
XX	WPI: 2001-442253/47.			
DR	N-PSDB: AAI58797.			
XX				
PT	Novel nucleic acids and polypeptides, useful for treating disorders			
PT	such as central nervous system injuries -			
XX				
XX	Example 4; SEQ ID NO 2786; 10078bp; English.			

CC	The invention relates to human nucleic acids (AA157798-AA161369) and
CC	the encoded polypeptides (AA38642-AA42213) with neurotropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC	utilisation of the activities such as: Immune system suppression,
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukemias and
CC	C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification.
SQ	Sequence 298 AA:
Query Match	94.0%; Score 1454; DB 22; Length 298;
Best Local Similarity	92.6%; Pred. No. 1.5e-144;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;	
QY	1 MFDALSFAPKDFLAGVAAATKTVAPRIERYKLLLOVOHASKOTITADKKYGIIDCYVR 60
DB	1 MTEGAISEFAKDFLAGGIAAATKTAVPARIERYKLLLOVOHASKOIAADKKYGIIDCIYR 60
QY	61 IPEKEDEVSEFMGNLANRYRFPQTALNPAFEDKKIQLFGVDKRTPQWRFEAGNLASG 120
DB	61 IPEKEGVSEFMGNLANRYRFPQTALNPAFEDKKIKQLFGVDKHDTQWRFAGNLASG 120
QY	121 GAAGATSLCEFYVLPDFAARTRLAADVGAKAGEREFGLGDCLVKIKYSDGINKLYOGFNWS 180
DB	121 GAAGATSLCEFYVPLDPARTRLAADVGSCTEREFGLDGCLVKIRKDSGIRLTYGGFSYS 180
QY	181 VGGIIITYRAARYIGITYDTAKGMLPDKRNTHIVISMMIACTVAVAGILTSPPFTVRRMMM 240
DB	181 VGGIIITYRAARYGVYDTAKGMLPDKRNTHIVISMMIACTVTAVAGVSYPFDVRRMMM 240
QY	241 GSGRGKTDMYTGTLDDCMWKRTARDGSGKAFFKGAMSNVLRGSGAFVLVLYDEIRK 296
DB	241 GSGRGKADIMYTGIVDCMKRIFRDGSGKAFFKGAMSNVLRGSGAFVLVLYDELKK 296
RESULT 6	
AAU01200	
ID	AAU01200 standard; Protein; 298 AA.
XX	AAU01200;
AC	
XX	07-SEP-2001 (first entry)
DE	
XX	Human adenine nucleotide translocator-3 (ANT-3) protein.
XX	
KM	Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
KW	mitochondrial permeability transition pore component; cell survival;
KM	mitochondrial core component; mitochondrial related disorder; cancer;
KW	Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX	
OS	Homo sapiens.
PN	WO200132876-AZ.
PD	10-MAY-2001.
XX	
PF	03-NOV-2000; 2000WO-US30535.
PR	03-NOV-1999; 99US-0434354.
XX	
PA	(MITO-) MITOKOR.
XX	
P1	Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Friegerl LG;


```

XX 22-OCT-2001 (first entry)
DF
XX
XX Human polypeptide SEQ ID NO 6358.
DE
XX
KW Human; neurotopic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
PN
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000MO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX
XX N-PSDB; AAI60583.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
XX Example 2; SEQ ID NO 6358; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX the encoded polypeptides (AAW38642-AAW42213) with neurotopic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemia and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX
XX Sequence 323 AA:
XX
XX Query Match 94.0%; Score 1454; DB 22; Length 323;
XX Best Local Similarity 92.6%; Pred. No. 1,7e-144;
XX Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0
XX
XX 1 MTDAAISFAMDFLAGGAAAIKSTAVAPIERVKLLQOVHASKQITADKQYKGIIDCVYR 60
XX ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX MTEQAIISFADDFLAGGIAAIKSTAVAPIERVKLLQOVHASKQIAADKQYKGIIDCVYR 85
XX
XX 61 IPKQEVLSFWRGRLAVIRYFPQALNFAFKRYKQIFLGGVDKRTQFPKRYFAGNLASG 120
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 86 IPKQGVLSFWRGRLAVIRYFPQALNFAFKRYKQIFLGGVDKRTQFPKRYFAGNLASG 145

```

OY 121 GAATATSLCFEYPLDPEAFRTLRADVCGAGAREFERELGDCIVKIKYSOSIKELXOGFNVN 180
 DB 146 GAAATSLSCFEYPLDPEAFRTLRADVCGSGEREFELGDCIVKIKYSOSIKELXOGFNVN 205
 OY 181 VGGIITVRAAFVGYIDFAKMGMLDPPKNTHTIVISMVIAQVTVAVAGLTSTPFPVTRRRMM 240
 DB 206 VGGIITVRAAFVGYIDFAKMGMLDPPKNTHTIVISMVIAQVTVAVAGVVSIPFPVTRRRMM 265
 OY 241 QSGRRKGDIMTGTGLDCWRKRIARDEGGKAFKFCAMSNVTRGMGAFVLYLDEIKK 296
 DB 266 QSGRRKGDIMTGTGDCWRKRIARDEGGKAFKFCAMSNVTRGMGAFVLYLDELKK 321
 RESULT 9
 ABG15423
 ID ABG15423 standard; Protein; 325 AA.
 XX
 AC ABG15423;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #15414.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN W0200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001MO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Drmanac RT, Liu C, Tang YT;
 DR WPI: 2001-639362/73.
 DR N-PSDB: AAS79610.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID No 45782; 103bp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

```

XX      Sequence      325 AA:
SQ      Query Match      91.6%; Score 1417; DB 22; Length 325;
      Best Local Similarity 92.7%; Pred. No. 1.4e-140;
      Matches 280; Conservative 3; Mismatches 15; Indels 4; Gaps 3;

OY      1 MTDAAISFPAKDFLAGVAAAIKSTAVAPIERVKLLLOVQHASKQITADKQYKGIIDCVR 60
      |||||.....|
DB      24 MTDAAVSFAKDFLAGVAAAIKSTAVAPIERVKLLLOVQHASKQIADKQYKGIIGCVR 83
OY      61 IPKEQEVLSFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQEFRRYFAGNLASG 120
      |||||.....|
DB      84 IPKEQGVLSFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQEFRRYFARNLASG 143
OY      121 GAAGATSLCFVYPLDFARTRLADVCGKAGAREFRGLDCLVKIYKSDGIGLYQGFNV 180
      |||||.....|
DB      144 GAAGATSLCFVYPLDFARTRLADVCGKAGAREFRGLDCLVKIYKSDGIGLYQGFNV 203
OY      181 VOGIIRYRAAYFGIYDTAKGMLPDPKNTHTIVISMIAQTY-TAVAGITSPEDT--VRRR 237
      |||||.....|
DB      204 VOGIIRYRAAYFGIYDTAKGMLPDPKNTHTIVISMIAQTYHCCPGXLPFPEDTRSVRN 263
OY      238 MMQSGRKGTDIWYTGTLDCMRKIADEGSKAFKFGKAMSVNLKMGCAFVLVLYD-EIKK 296
      |||||.....|
DB      264 EXMQSGRKGTDIWYTGTLDCMRKIADEGSKAFKFGKAMSVNLKMGCAFVLVLYEXSKR 323
OY      297 YT 298
      ||
DB      324 YT 325

RESULT 10
AAM61169
ID      AAM61169 standard; Protein: 298 AA.
XX
AC      AAM61169;
XX
DT      28-SEP-1998 (first entry)
XX
DE      Anti protein.
XX
KW      Anti; Adenine nucleotide translocator; cloning; screening;
KW      DNA Tag diexoxy terminator cycle sequencing; oxidative phosphorylation;
KW      probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
KW      hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
KW      lactic acidosis; degenerative muscle disease.
XX
OS      Mus sp.
XX
PN      WO9819714-A1.
XX
PD      14-MAY-1998.
XX
PF      31-OCT-1997; 97WO-US19882.
XX
PR      01-NOV-1996; 96US-0030017.
XX
PA      (UYEM-) UNIV EMORY.
XX
PI      Graham BC, Macgregor GR, Wallace DC;
XX
DR      MPI: 1998-286608/25.
DR      N-PSDB; AAV36479.
XX
XX      Mice lacking heart-muscle adenine nucleotide translocator protein -
PT      useful as model for mitochondrial myopathy and hypertrophic
PT      cardiomyopathy in animals and to test therapeutic compositions or
PT      gene therapies
XX
PS      Disclosure: Page 39-40; 61pp; English.
XX
XX      The present sequence is the mouse Anti protein, the cDNA producing this
CC

```

```

CC      polypeptide is cloned by screening a mouse heart cDNA library with the
CC      human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA
CC      Tag diexoxy terminator cycle sequencing. The Anti protein is encoded by
CC      the Anti locus, a nuclear gene on chromosome 8. This protein is required
CC      in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
CC      which can then be converted into ATP. An Anti homozygous mutant would
CC      thus be defective in OXPHOS which results in disease in oxidative
CC      metabolism dependent tissues. This mouse Anti homozygous mutant can be
CC      used as a model system for fascioscapular humeral muscular dystrophy,
CC      hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
CC      systems can be used to test possible therapeutic compounds which
CC      increase/mediate ATP and ADP exchange across the mitochondrial membrane
CC      independent of ANTI.
XX
SQ      Sequence      298 AA:
      Query Match      91.2%; Score 1411; DB 19; Length 298;
      Best Local Similarity 89.2%; Pred. No. 5.2e-140;
      Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

OY      1 MTDAAISFPAKDFLAGVAAAIKSTAVAPIERVKLLLOVQHASKQITADKQYKGIIDCVR 60
      |||||.....|
DB      1 MTDAAISFPAKDFLAGVAAAIKSTAVAPIERVKLLLOVQHASKQISAEKQYKGIIDCVR 60
OY      61 IPKEQEVLSFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQEFRRYFAGNLASG 120
      |||||.....|
DB      61 IPKEQGVLSFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQEFRRYFAGNLASG 120
OY      121 GAAGATSLCFVYPLDFARTRLADVCGKAGAREFRGLDCLVKIYKSDGIGLYQGFNV 180
      |||||.....|
DB      121 GAAGATSLCFVYPLDFARTRLADVCGKAGAREFRGLDCLVKIYKSDGIGLYQGFNV 180
OY      181 VOGIIRYRAAYFGIYDTAKGMLPDPKNTHTIVISMIAQTYTAVAGLTSYFPDTRRRMM 240
      |||||.....|
DB      181 VOGIIRYRAAYFGIYDTAKGMLPDPKNTHTIVISMIAQTYTAVAGLTSYFPDTRRRMM 240
OY      241 QSGRKGTDIWYTGTLDCMRKIADEGSKAFKFGKAMSVNLKMGCAFVLVLYDEIKKY 297
      |||||.....|
DB      241 QSGRKGTDIWYTGTLDCMRKIADEGSKAFKFGKAMSVNLKMGCAFVLVLYDEIKKY 297

RESULT 11
AAV71031
ID      AAV71031 standard; Protein: 297 AA.
XX
AC      AAV71031;
XX
DT      29-AUG-2000 (first entry)
XX
DE      Human adenine nucleotide translocator ANTI.
XX
KW      Human; adenine nucleotide translocator; ANTI; mitochondria; ADP; ATP;
KW      adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW      mitochondrial permeability transition; neuroprotective; noctropic;
KW      antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW      antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
KW      Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW      diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW      mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW      mitochondrial diabetes and deafness; hyperproliferative disorder;
KW      myoclonic epilepsy red ragged fibre syndrome.
XX
OS      Homo sapiens.
XX
PN      WO200026370-A2.
XX
PD      11-MAY-2000.
XX
PF      03-NOV-1999; 99WO-US25883.
XX
PR      03-NOV-1998; 98US-0185904.
PR      08-SEP-1999; 99US-0393441.
XX
XX

```

PA (MITO-) MITOKOR.
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX
XX WPI: 2000-365619/31.
DR N-PSDB: AAD00519.
XX
XX Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
XX Claim 44: Page 172; 175pp: English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MTDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT1 from human brain.
XX
XX Sequence 297 AA;
SQ
Query Match 89.9%; Score 1391.5; DB 21; Length 297;
Best Local Similarity 88.6%; Pred. No. 5.9e-138;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MTDALSFAPKDFLAGVAAAIKSTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
Db 1 MGDHAWMSFLKDFLAGVAAVAASKTAVAPIERVKLLQVHASKQISAKQYKGIIDCVVR 60
QY 61 IPKDEVSLFWKGNLANVIRFPFOALNFAFKDKYKQJFLGVDVKRTOFWMYFAGNLSG 120
Db 61 IPKDEGSLFWKGNLANVIRFPFOALNFAFKDKYKQJFLGVDVRHKKFWMYFAGNLSG 120
QY 121 GAAGATSLCFYVPLDFARTRLAADYGKAGAREFRGLDCLVKTIYKSGITGLVQGFNVS 180
Db 121 GAAGATSLCFYVPLDFARTRLAADYGR-AQREFHGLDCLTIKFSGLGLVQGFNVS 179
QY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTNHIYSWMIAGTVAAGLTSYPPDYVRRMM 240
Db 180 VOGIIIRAAVFGIYDTAKGMLPDPKNVHIFVSWMIAOSVAVAGLLSYPPDYVRRMM 239
QY 241 QSGRKGTDIMYTGTLDCRKRTARDEGKAFKAGMSNVLRMGAFVLYLDEIKKY 297
Db 240 QSGRKGADIMYTGVDCKRIAKDEGAKAFKAGMSNVLRMGAFVLYLDEIKKY 296
RESULT 12
AAU01198
ID AAU01198 standard; Protein: 297 AA.
XX
XX AAU01198;
AC
XX
XX 07-SEP-2001 (first entry)
DE Human adenine nucleotide translocator-1 (ANT-1) protein.
XX
XX Human adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX
XX Homo sapiens.
OS
XX WO200132876-A2.
PN
XX 10-MAY-2001.
PD
XX 03-NOV-2000; 2000WO-US30535.
PF
XX 03-NOV-1999; 99US-0434354.
PR
XX
XX (MITO-) MITOKOR.
PA
XX
XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
PI Velicic G, Davis RE;
PI WPI: 2001-291054/30.
DR N-PSDB: AAS05901.
XX
XX New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
XX Disclosure: Fig 2; 186pp: English.
XX
XX The present sequence represents human adenine nucleotide translocator-1
CC (ANT-1) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLAHS sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
XX Sequence 297 AA;
SQ
Query Match 89.9%; Score 1391.5; DB 22; Length 297;
Best Local Similarity 88.6%; Pred. No. 5.9e-138;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MTDALSFAPKDFLAGVAAAIKSTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
Db 1 MGDHAWMSFLKDFLAGVAAVAASKTAVAPIERVKLLQVHASKQISAKQYKGIIDCVVR 60
QY 61 IPKDEVSLFWKGNLANVIRFPFOALNFAFKDKYKQJFLGVDVKRTOFWMYFAGNLSG 120
Db 61 IPKDEGSLFWKGNLANVIRFPFOALNFAFKDKYKQJFLGVDVRHKKFWMYFAGNLSG 120
QY 121 GAAGATSLCFYVPLDFARTRLAADYGKAGAREFRGLDCLVKTIYKSGITGLVQGFNVS 180
Db 121 GAAGATSLCFYVPLDFARTRLAADYGR-AQREFHGLDCLTIKFSGLGLVQGFNVS 179
QY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTNHIYSWMIAGTVAAGLTSYPPDYVRRMM 240
Db 180 VOGIIIRAAVFGIYDTAKGMLPDPKNVHIFVSWMIAOSVAVAGLLSYPPDYVRRMM 239
QY 241 QSGRKGTDIMYTGTLDCRKRTARDEGKAFKAGMSNVLRMGAFVLYLDEIKKY 297
Db 240 QSGRKGADIMYTGVDCKRIAKDEGAKAFKAGMSNVLRMGAFVLYLDEIKKY 296

```
RESULT 13
AAU10378
ID AAU10378 standard; Protein; 297 AA.
XX
AC AAU10378;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human adenine nucleotide translocator 1 (ANT1).
XX
KW Human: adenine nucleotide translocator; ANT;
KW mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
PN MO200185944-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-US15416.
XX
PR 11-MAY-2000; 2000US-0569327.
XX
PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
XX
DR WPI; 2002-055598/07.
DR N-PSDB; AAS16688.
XX
PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide
XX
XX Claim 44; Fig 2; 147pp; English.
XX
CC The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT1.
XX
XX Sequence 297 AA:
XX
Query Match 89.9%; Score 1391.5; DB 23; Length 297;
Best Local Similarity 88.6%; Pred. No. 5.9e-138;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
OY 1 MTEAALSFADFLAGVAAAIKSTAAVPIERVKLLLOVQASHKOITADKOYKGIIDCVNR 60
OY 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 MGHAMSFLLKDFLAGVAAVAASKTAAVPIERVKLLLOVQASHKOISAEKYGKGIIDCVNR 60
OY 61 IPKEQEVLSFWRGNLNAVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRRFAGNLASG 120
OY 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 61 IPKEQGLISFWRGNLNAVIRYPTQALNFAFKDKYKQLFLGVDHRKQFWRRFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTLADVCAKAGAEFERRGIDGLVITRKSDGIRKGLYOGNNVS 180
OY 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 121 GAAGATSLCFVYPLDFARTLADVGNR-AQREFHGLGDCIIRIKFSKDLRGLYOGNNVS 179
```

```
OY 181 VGGIIIRAAVFGIYDTAKGMLPDPKNTTHIVISWMIQOTVAVAGLSTYFPDVRRRMM 240
OY 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 180 VGGIIIRAAVFGIYDTAKGMLPDPKNTTHIVISWMIQOTVAVAGLSTYFPDVRRRMM 239
OY 241 QSGRKGTDIMYTGLDCMRRIARDEGKAFFKGAMSVNLKMGCAFVLVYDEIKKY 297
OY 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 240 QSGRKGADIMYTGTVDCKRIARDEGAKAFKGAAMSVNLKMGCAFVLVYDEIKKY 296
RESULT 14
ABG27056
ID ABG27056 standard; Protein; 263 AA.
XX
AC ABG27056;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27047.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN MO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS91243.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
XX Claim 20; SEQ ID No 57415; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
XX
XX Sequence 263 AA:
XX
Query Match 87.0%; Score 1346; DB 22; Length 263;
Best Local Similarity 99.2%; Pred. No. 3.1e-133;
```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:25 ; Search time 11.6797 Seconds

(without alignments)
750.705 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547

Sequence: 1 MTDALSFADFLAGVAA.....LRGGAFLVLYDEIKKYT 298

Scoring table:

BIOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/p/tdatata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/p/tdatata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/p/tdatata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/p/tdatata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/p/tdatata/1/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/p/tdatata/1/1aa/backfilltest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1411	91.2	298	US-08-961-871-10	Sequence 10, Appl
2	301	19.5	469	US-09-188-930-339	Sequence 339, App
3	274	17.7	291	US-09-501-558-2	Sequence 2, Appl
4	261.5	16.9	447	US-09-160-119-4	Sequence 4, Appl
5	261.5	16.9	674	US-09-160-119-2	Sequence 2, Appl
6	247	16.0	312	US-09-142-565-2	Sequence 2, Appl
7	244.5	15.8	311	US-08-775-009-33	Sequence 3, Appl
8	239.5	15.5	309	US-08-518-878B-51	Sequence 51, Appl
9	239.5	15.5	309	US-08-807-861A-51	Sequence 51, Appl
10	239.5	15.5	309	US-08-470-868A-51	Sequence 51, Appl
11	239.5	15.5	309	US-09-210-681-51	Sequence 51, Appl
12	239.5	15.5	309	US-08-946-719A-51	Sequence 56, Appl
13	236.5	15.3	299	US-08-518-878B-56	Sequence 56, Appl
14	236.5	15.3	299	US-08-470-868A-56	Sequence 32, Appl
15	232.5	15.0	311	US-08-775-009-32	Sequence 32, Appl
16	230.5	14.9	320	US-08-933-750C-12	Sequence 12, Appl
17	230.5	14.9	320	US-09-234-613-12	Sequence 12, Appl
18	227	14.7	308	US-08-937-466-2	Sequence 2, Appl
19	227	14.7	308	US-09-172-528-2	Sequence 2, Appl
20	227	14.7	308	US-09-318-199-2	Sequence 2, Appl
21	227	14.7	308	US-09-503-579-2	Sequence 2, Appl
22	223	14.4	432	US-08-937-466-4	Sequence 4, Appl
23	223	14.4	432	US-09-172-528-4	Sequence 4, Appl
24	223	14.4	432	US-08-946-719A-56	Sequence 4, Appl
25	223	14.4	432	US-09-318-199-4	Sequence 4, Appl
26	219.5	14.2	293	US-09-501-558-4	Sequence 4, Appl
27	218.5	14.1	303	US-08-294-532B-36	Sequence 36, Appl

28	217.5	14.1	303	US-08-518-878B-37	Sequence 37, Appl
29	217.5	14.1	303	US-08-807-861A-37	Sequence 37, Appl
30	217.5	14.1	303	US-08-470-868A-37	Sequence 37, Appl
31	217.5	14.1	303	US-09-210-681-37	Sequence 37, Appl
32	217.5	14.1	303	US-08-946-719A-37	Sequence 37, Appl
33	191	12.3	328	US-09-068-140A-15	Sequence 15, Appl
34	190.5	12.3	256	US-08-937-466-6	Sequence 6, Appl
35	190.5	12.3	256	US-09-172-528-6	Sequence 6, Appl
36	190.5	12.3	256	US-09-318-199-6	Sequence 6, Appl
37	190.5	12.3	256	US-09-503-579-6	Sequence 6, Appl
38	189	12.2	306	PCT-US94-09799-1	Sequence 1, Appl
39	187.5	12.1	307	US-08-807-861A-56	Sequence 56, Appl
40	187.5	12.1	307	US-09-210-681-56	Sequence 56, Appl
41	187.5	12.1	307	US-08-946-719A-56	Sequence 56, Appl
42	187	12.1	351	US-08-933-750C-19	Sequence 19, Appl
43	187	12.1	351	US-09-234-613-19	Sequence 19, Appl
44	181	11.7	289	US-09-068-140A-10	Sequence 10, Appl
45	173.5	11.2	312	US-09-188-930-142	Sequence 142, App

ALIGNMENTS

RESULT 1
US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Macgregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10
Query Match 91.2%, Score 1411, DB 3, Length 298;
Best Local Similarity 89.2%, Pred. No. 2.8e-154;
Matches 265, Conservative 15, Mismatches 17, Indels 0, Gaps 0;
OY 1 MTDALSFADFLAGVAAISKTAVERKLLQVQHSKQITADKQYGIIDCVVR 60

```
Db      1 MGQALSPFKDLAGGIAAASVTAAVPIERVLLQVOHASKQIAEKQKGIIDCV 60
Qy      61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKOIFLGGVDKRTQFWRYPAGNLAG 120
Db      61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKOIFLGGVDKRTQFWRYPAGNLAG 120
Qy      121 GAAGATSLCFVYPLDFARTRLADVGKAGAEERERGLDGLVYKYSKGIGLYOGFNVS 180
Db      121 GAAGATSLCFVYPLDFARTRLADVGKAGAEERERGLDGLVYKYSKGIGLYOGFNVS 180
Qy      181 VQGIITIRAAVFGIYDTAGMLPDPKNTHTVISMIAQIYTAAGITSPFDIVRRMM 240
Db      181 VQGIITIRAAVFGIYDTAGMLPDPKNTHTVISMIAQIYTAAGITSPFDIVRRMM 240
Qy      241 QSGRKGTDIMYTGTLDCKRKIADEGKAFKFGKAGSNVLKMGAFVLYDEIKKY 297
Db      241 QSGRKGTDIMYTGTLDCKRKIADEGKAFKFGKAGSNVLKMGAFVLYDEIKKY 297
```

RESULT 2

US-09-188-930-339

Sequence 339, Application US/09188930A

Patent No. 6150502

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Onrust, Rene

APPLICANT: Murlson, James Greg

TITLE OF INVENTION: Compositions Isolated From Skin Cells

TITLE OF INVENTION: and Methods For Their Use

FILE REFERENCE: 11000.1011c1

CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 339

LENGTH: 469

TYPE: PRT

ORGANISM: Mouse

US-09-188-930-339

Query Match

19.5%; Score 301; DB 4; Length 469;

Best Local Similarity 28.4%; Pred. No. 5e-26;

Matches 86; Conservative 62; Mismatches 109; Indels 46; Gaps 12;

```
Qy      10 KDFLAGVAAATSKTAVAPIERVKLLQVOHASKQITADKQYGIIDCV-----RIPKEQ 65
Db      188 RHLVAGGGAASRTCTAPLRLKVLMOY-HASRSNNM-----CIVGFTQMIREG 237
Qy      66 EVLSFWRGNLANVIRYPTQALNFAFKDKYKOIFLGGVDKRTQFWRYPAGNLAGSAGA 125
Db      238 GAKSLMRGNINVLKTAIPESAIKFMAYEQMKR--LVGSOET---LRHERLVAGSLAGA 292
Qy      126 TSLCFVYPLDFARTRLADVGKAGAEERERGLDGLVYKYSKGIGLYOGFNVSVOGII 185
Db      293 IQOSSYIPMEVLTTRMA--LRKTG---QYSGMLDCARILAEKGVAAFYKGYIPNMLGIT 347
Qy      186 IYRAAFYGYIDRAKGLPDPKNTHTVISMIAQIYTAAG--LTSYPTPT 233
Db      348 PYAGIDLAYEYL-----KNTWLDORYVNSADPGVYLLACGTISSYCGQLASTYPLAL 400
Qy      234 VRRMMQSGRKGTDMYTGTLDCKRKIADEGKAFKFGKAGSNVLKMGAFVLYDEIKKY 292
Db      401 VTRFMQAGASIEGAPRYTMSL--FKQILTBESAGLKYGLAPNFKVLPANVSISTYVIE 458
Qy      293 EIK 295
Db      459 NLK 461
```

*RESULT 3

```
US-09-501-558-2
Sequence 2, Application US/09501558
Patent No. 6403784
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0012-USA
CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 291
TYPE: PRT
ORGANISM: Homo sapiens
US-09-501-558-2
```

Query Match

17.7%; Score 274; DB 4; Length 291;

Best Local Similarity 27.8%; Pred. No. 3.1e-23;

Matches 85; Conservative 55; Mismatches 134; Indels 32; Gaps 9;

```
Qy      4 AALSPAFKDFLAGGVAATSKTAVAPIERVKLLQVOHAS-----KQITADKQYGIIDCV 58
Db      2 SALNM--KPFVYGGSLATITACGFFPIDLKTRLQIGQINDAKFKFI-----HYRGLMHL 56
Qy      59 VRIPEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKOIFLGGVDKRTQFWRYPAGNLA 118
Db      57 VRIGREGKALYSGTAPMLRLQASGTIKIGTOSLKRFLTERPDET-----LPINVI 111
Qy      119 SGGAATSLCFVYPLDFARTRLADVGKAGAEERERGLDGLVYKYSKGIGLYOGFN 178
Db      112 CGILSVISSTIANPYDITKIRMQAOSNTIG-----GIGNPMNITYQDETRGLMKVP 166
Qy      179 VSVQGIITIRAAVFGIYDTAK-----GMLPDPKNTHTVISMIAQIYTAAGITSPPD 232
Db      167 LTAQRAIYVGVLPYDITKRLILSLGMDIVYTHFLSF-----TCLAGLANSNPD 222
Qy      233 TVRRMMQSG--RKGTDMYTGTLDCKRKIADEGKAFKFGKAGSNVLKMGAFVLYL 290
Db      223 VVTRMMNOVRLDGRGSGYGTLDCLQTWKNEGFALYKGFPMWRLGPMNITFEVT 282
Qy      291 YDEIK 296
Db      283 YEQLR 288
```

RESULT 4

US-09-160-119-4

Sequence 4, Application US/09160119A

Patent No. 6316219

GENERAL INFORMATION:

APPLICANT: KRIEF, STEPHANE

APPLICANT: SOUCHEP, MICHEL

APPLICANT: BRIL, ANTOINE

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GH-30985

CURRENT APPLICATION NUMBER: US/09/160,119A

CURRENT FILING DATE: 1998-09-24

EARLIER APPLICATION NUMBER: EP 97402511.6

EARLIER FILING DATE: 1997-10-23

EARLIER APPLICATION NUMBER: EP 98401655.0

EARLIER FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 447

TYPE: PRT

ORGANISM: HOMO SAPIENS

US-09-160-119-4

[illegible]

```

RESULT 5
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PR1
; ORGANISM: HOMO SAPIENS
; US-09-160-119-2

Query Match      16.9%; Score 261.5; DB 4; Length 674;
Best Local Similarity 26.2%; Pred. No. 3.2e-21;
Matches 77; Conservative 51; Mismatches 139; Indels 27; Gaps 7

OY   12 FLAGVAAAIKSTAVAPLERVKLLQVQHASKQTADKOYKGIIDCVARIPKEQEVLSFW 71
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db   331 FGLSVAAGAVATAYPRDLVKTRQONORSTGSEFGEIIVAKNSPFCFKVLRYEGFFGLY 390
OY   72 RGNLANTVGRPEPTQALNFAFKDYKQIFL---GGVDKRTPQFRVPFAGNLASGAGATSL 128
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db   391 RGLLRQLLGVARPERKIKTLVNDFVADKRMHKDGSVP-----LAELIAGCAGSGOV 442
OY   129 CFVVPLDFARTRLRADVGKAGAEERFGISGLDCLVKITYSDGIGKLGYGFENSVQGIIIR 188
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db   443 IFTNPLELVKIRLQV-----AGEITTGPRVSALSUVNRDLGFFGAIKGAACFLRDIPFS 496
OY   189 AAFEGTYDTAKGMPLDDPKNTHTIVISMTIAQVTAAVAGLTS----VPEDVRRRMMOSQR 244
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db   497 AIIEPCYAHVKAASFNNEGQVSPGSLULA--GALAGMPAASLVYPADVIKTR--LQVAA 551
OY   245 KGTDIMTGTGLDCWKRIARDEGKAEFFKGAMSNVLRGMGQ-AFVLVLXDRIKKY 297
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db   552 RAGQTTYSVIDCFEKRIIREEGPRLMKMGAGARVRPSSPFQGVLTLLTYELLORM 605

```

```

RESULT 6
US-09-142-565-2
: Sequence 2, Application US/09142565A
: Patent No. 6187560
: GENERAL INFORMATION:
: APPLICANT: Lee James Beeley
: APPLICANT: Kelly Paine
: APPLICANT: Robert James
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GH-30002
: CURRENT APPLICATION NUMBER: US/09/142,565A
: CURRENT FILING DATE: 1999-06-30
: EARLIER APPLICATION NUMBER: 9704551.2
: EARLIER FILING DATE: 1997-03-05
: EARLIER APPLICATION NUMBER: 9705614.7
: EARLIER FILING DATE: 1997-03-18
: EARLIER APPLICATION NUMBER: 97305305.1
: EARLIER FILING DATE: 1997-07-16
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 312
: TYPE: PRT
: ORGANISM: HOMO SAPIEN
US-09-142-565-2

```

```

Query Match Similarity      16.0%: Score 247; DB 4; Length 312;
Best Local Similarity      24.8%: Pred. No. 4.5e-20;
Matches 76; Conservative 56; Mismatches 149; Indels 26; Gaps 8

QY      2 TDAALSPFAKDFLAGGVAALISKTAAPIERVYKLLLOVQHASKOITADK--QYKGIIDCV 59
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Db      7 SDVPPTMAVKFLGACTACGADLAFPEPDTAKVRIGIOENQAVQARLVQYRGVIGITL 66
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
QY      60 RLPKQDEVLSTPRKGLANVIRYFPFOALNFAFKDKYKQIFL--GVDYKRPQFMYRFAGNLA 118
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Db      67 TMRREGPCSPYNGIVAGIQROMSPASIRIGLIDYSKQYVTFPKGADNSLTTRILA---- 122
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
QY      119 SGGAAGATSLCIVVYPLDFARTRLADV--GKAAGEHEPFGIDCLVKKYKSDGIKGLYOG 176
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Db      123 -GCTTGAAMAVTCAOFTDYVVKVRFQASIHIGPFRSDRKYSTGMDAYRTIAREGCVRLMKWG 181
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
QY      177 FNVSVQGIIRAAVFGIYDPAK-----GMLPDPKNTHIVISMIAQVTAVAGLTSTYP 230
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Db      182 TLPINRMAIVCAEVYVYTDILKEKLLDYHLLTDNPPCFHVSAGFCATVVAS----P 237
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
QY      231 FDTVRRRMMSGRRGCTDIMGTLDDCKRKIKARDGGRKAFEGFGAMSNVLR--GMGGAFVLV 289
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Db      238 VDVVTRRYM-----NSPPQGYFSPIDCKMKVAQEGPAFYKGFPPSPFLRLGSMNVYMEV 292
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
QY      290 LYDEIKK 296
      1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Db      293 TYEQLR 299

RESULT 7
US-08-775-009-33
: Sequence 33, Application US/08775009
: Patent No. 5935783
: GENERAL INFORMATION:
: APPLICANT: Gong, Wellong
: APPLICANT: Emanuel, Beverly S.
: APPLICANT: Budarf, Marcia L.
: APPLICANT: Roe, Bruce
: TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
: TITLE OF INVENTION: Velocardiofacial Syndrome Minimal Critical Region
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
: ADDRESSEE: NO. 5935783ris, LLP
: STREET: One Liberty Place - 46th Floor

```


APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-807-861A-51

Query Match 15.5%; Score 239.5; DB 2; Length 309;
Best Local Similarity 23.5%; Pred. No. 3.2e-19;
Matches 72; Conservative 58; Mismatches 149; Indels 27; Gaps 8;

QY 2 TDAALSFADKDLGAGVAAAIKSTAVAPIERVKLLQVOHASK---QIADKQYKGIIDCV 58
DB 7 TDVPTATVVKRLGAGTACIADLITFPLDTAKVRLQIGESGCPVRAVSQYKGMGTI 66
QY 59 VRIPEQEVLSFWRGNLANVIRYFTQALNFAFDKRYQIFLGVDKRTCFWRRFAGNLA 118
DB 67 LTMWTEGPRSLYNGLVAGLQROMSFASVRIGLDVSKQFYTKGSEHAS-----IGSRL 121
QY 119 SGGAAGATSLCFVYPLDPAFTRRLADVGKAGAEFRGLGCLVITYSDGIKGLYGFN 178
DB 122 AGSTTGALAAVAAOPTDVVKVRFQAO-ARAGGRRYQSTVNAKYKTIAREEGFRGLMKGT 180
QY 179 VSVQGIITRYAAVFGIYDTAK-----GMLPDPKNTHTIVISMIAQVTAAVAGLTSYFPD 232
DB 181 PNVARNAIVNCAELVLYLIDALLKANIMTDLPCHFTSAFGAGFCFTVIAS----PVD 236
QY 233 TVRRRMQMOS-GRKGTDMYTGTLDCMKRIARDEGKAFFGANSNVL-R-GMGAFVLYL 290
DB 237 VVKTRYNSALGQ-----YSSAGHCALTMLOKEGPRAFYKGFMPSEFLRLGSMNVMEVT 290
QY 291 YDEIKK 296
DB 291 YEQLKR 296

RESULT 10
US-08-470-868A-51
Sequence 51, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-51

Query Match 15.5%; Score 239.5; DB 2; Length 309;
Best Local Similarity 23.5%; Pred. No. 3.2e-19;
Matches 72; Conservative 58; Mismatches 149; Indels 27; Gaps 8;

QY 2 TDAALSFADKDLGAGVAAAIKSTAVAPIERVKLLQVOHASK---QIADKQYKGIIDCV 58
DB 7 TDVPTATVVKRLGAGTACIADLITFPLDTAKVRLQIGESGCPVRAVSQYKGMGTI 66
QY 59 VRIPEQEVLSFWRGNLANVIRYFTQALNFAFDKRYQIFLGVDKRTCFWRRFAGNLA 118
DB 67 LTMWTEGPRSLYNGLVAGLQROMSFASVRIGLDVSKQFYTKGSEHAS-----IGSRL 121
QY 119 SGGAAGATSLCFVYPLDPAFTRRLADVGKAGAEFRGLGCLVITYSDGIKGLYGFN 178
DB 122 AGSTTGALAAVAAOPTDVVKVRFQAO-ARAGGRRYQSTVNAKYKTIAREEGFRGLMKGT 180
QY 179 VSVQGIITRYAAVFGIYDTAK-----GMLPDPKNTHTIVISMIAQVTAAVAGLTSYFPD 232
DB 181 PNVARNAIVNCAELVLYLIDALLKANIMTDLPCHFTSAFGAGFCFTVIAS----PVD 236
QY 233 TVRRRMQMOS-GRKGTDMYTGTLDCMKRIARDEGKAFFGANSNVL-R-GMGAFVLYL 290
DB 237 VVKTRYNSALGQ-----YSSAGHCALTMLOKEGPRAFYKGFMPSEFLRLGSMNVMEVT 290
QY 291 YDEIKK 296
DB 291 YEQLKR 296

RESULT 11
US-09-210-681-51
Sequence 51, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/09/210,681
3 FILING DATE:
4 CLASSIFICATION:
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 08/807,861
7 FILING DATE: 26-FEB-1997
8 APPLICATION NUMBER: US 08/518,878
9 FILING DATE: 23-AUG-1995
10 APPLICATION NUMBER: US 08/470,868
11 FILING DATE: 06-JUN-1995
12 APPLICATION NUMBER: US 08/294,522
13 FILING DATE: 23-AUG-1994
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Coruzzi, Laura A.
16 REGISTRATION NUMBER: 30,742
17 REFERENCE/DOCKET NUMBER: 7853-066
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (212) 790-9090
20 TELEFAX: (212) 869-9741/8864
21 TELEX: 66141 PENNIE
22 INFORMATION FOR SEQ ID NO: 51:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 309 amino acids
25 TYPE: amino acid
26 STRANDEDNESS: single
27 TOPOLOGY: unknown
28
29 US-09-210-681-51

```

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,719A
FILING DATE: 8-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:

Query Match Similarity	15.5%	Score 239.5	DB 3	Length 309
Best Local Similarity	23.5%	Pred. No. 3,2e-19		
Matches	72	Conservative	58	Mismatches 149
			Indels	27
			Gaps	

QY	2	TDALSPAKDLTAGVA	AAISTAVAPIERVKLLQVQHASK--QITADKQYKGIIDCV	58
DB	7	TDVPTATVAKFLPGAT	TAACIADLITPELDTAKVRLOIQEESOGPAVATVSADQRCVMGTI	66
QY	59	VAIPKEOEVLSPWRGN	LNAVIRYPTQALNFAFKKRYKQIFLGQGVNKKRQPMRFAGNLTA	118
DB	67	LTMVTEGRSLYXNGL	YVAGLQROMSFASVRIGLYDSVKQFYTKGSHAS-----IGSRLL	121
QY	119	SGGAAGATSLCFVPL	DLFARTRLADVGCAGAREFERGLGDCLVIKYSDGIKGLYGFN	178
DB	122	AGSTTGALAVAAOCP	TDVVKVRFQAO-AAGGGRRYOSTVNAVYKTTIAREEGFRGLMKGT	180
QY	179	VSVOGIITRYRAYF	GIYDPK-----GMLPDKNTHIYSNMIAQTVAAVGLTSPD	232
DB	181	PVAVNNAIYNCELVT	YDILKDALKANLMTDDLPCHFISAGAGCTIVAS----PVD	236
QY	233	TYRRRMAMOS-GRK	GTIDMYTGTLDCKIRIADDEGKAFKGAWSVLR-GMGAGFVLYL	290
DB	237	VKTYTYMNSALQ----	YSSAGHCALTMLOKEGFRAYYKGFMSFRLRSGSNVVMFYT	290
QY	291	YDEIKK	296	
DB	291	YEQLRK	296	

RESULT 12
US-08-946-719A-51
Sequence 51, Application US/08946719A
Patent No. 6121017
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.,
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

```

; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-08-946-719A-51

Query Match          15.5%; Score 239.5; DB 3; Length 309;
Best Local Similarity 23.5%; Pred. No. 3,2e-19;
Matches 72; Conservative 58; Mismatches 19; Indels 27; Gaps 8;

QY      2 TDALISFKDPLAGVAANAISKTAAPLEPERVKLLLOVQHASK---QTADKQYGIIDCV 58
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db       7 TDPVPATAVKFLGASTAACIADLTFFPDLTAKVRQLQIGESOGPYRAVSQAQRYGMGTI 66
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |

QY      59 VRIPEKECEVLSEFMRGNLANVIREFPTQALNFAFKKYQFIQGLGVDRKTQCFRPFAGNLA 118
        :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db       67 LTMWTEGPRLSYNLGNLTVAGLQRKMSFASVRIGLYDSVKQFTKGSEHAS-----IGSRLL 121
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |

QY      119 SGGAAGAISLCFVYPLDPAFRTRLADYKAKAEERFRLGDCLVKITYSDGIKGYGFN 178
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db       122 AGSTTGALAVALVAOQPTDVVKVFQAO -ARAGGRRYOSTVNAYKTTIAEEBGRGLMKTGS 180
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |

QY      179 VSVOGIITRYRAYEGSIYDTAK-----GMLDDPKNTHTIVISMIAQVTAVAGLSYPED 232
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db       181 PNVARNALVNCAELVTDYLKDALLKANLMMDLDCHP TSAFGAGFCCTVIAS-----EVD 236
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |

QY      233 TVRRMMMQS-GRKSTDIMTYGTILDCKMKIARDDEGKAFFPGAMSNVLR -GMGCAFVLYL 290
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db       237 VKTRYNNMSALGO-----YSSAGHCALTMLQKEBPRAFYRGFMPSFLRLSMNVVMFEV 290
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |

QY      291 YDEIKR 296
        |::|:
Db       291 YEOLKR 296

RESULT 13
US-08-518-878B-56
; Sequence 56, Application US/08518878B
; Patent No. 5702802
; GENERAL INFORMATION:
; APPLICANT: Tartagila, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-56

```

```

Query Match 15.38; Score 236.5; DB 1; Length 299;
Best Local Similarly 23.6%; Pred. No. 6.8e-19;
Matches 70; Conservative 57; Mismatches 142; Indels 27; Gaps 8;

OY 12 FLAGVAAAIKTAIVAPIERVKLLVOYHASK---QITADKQYGIIDCVIRIKEDVL 68
DB 7 FLGAGTACIADLTTFPDTAKVRLQIGESQGPVATSAQYKGMGTITLWRTESPR 66
OY 69 SFWRGNLANVIRYPTTALNFAFDKQKQIFLGVDKRTQFWRFYAGNLASGAAGATSL 128
DB 67 SLVNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHNS-----IGSLLAGSTTGALAV 121
OY 129 CFVYPDEPARKRLADYDKAGAREFRGLDCLVKYIKSDIKLYOGFNVSVGCIITYYR 188
DB 122 AVAOPTVVKKYRFQAO--ARAGGRRYOSTVNAVYRTIAEEGFRGLMGKTSFNVARNALVN 180
OY 189 AAYGIVDTAK-----GMLPDPKNTFHVISMIAQVTVAVAGLTSVPFDTVRRMMQOS 242
DB 181 CAELVTYDLIKDALKANLMTDLPCHFTSAFGAGFCTTYVAS----PVDVYKTRYMNSA 236
OY 243 -GRKGTIMYTGTLDCWKRRIARDEGKAFFKGANSNVLK--GMGAFVLYLYDEIK 296
DB 237 LGQ-----YSSAGHCALTMLOKEGPRAFYKGFMPSPFLRLGSMVMVMEVTEYQLKR 286

```

```

RESULT 14
US-08-470-868A-56
Sequence 56, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-56

```

```

Query Match 15.38; Score 236.5; DB 2; Length 299;
Best Local Similarly 23.6%; Pred. No. 6.8e-19;
Matches 70; Conservative 57; Mismatches 142; Indels 27; Gaps 8;

OY 12 FLAGVAAAIKTAIVAPIERVKLLVOYHASK---QITADKQYGIIDCVIRIKEDVL 68
DB 7 FLGAGTACIADLTTFPDTAKVRLQIGESQGPVATSAQYKGMGTITLWRTESPR 66
OY 69 SFWRGNLANVIRYPTTALNFAFDKQKQIFLGVDKRTQFWRFYAGNLASGAAGATSL 128
DB 67 SLVNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHNS-----IGSLLAGSTTGALAV 121
OY 129 CFVYPDEPARKRLADYDKAGAREFRGLDCLVKYIKSDIKLYOGFNVSVGCIITYYR 188
DB 122 AVAOPTVVKKYRFQAO--ARAGGRRYOSTVNAVYRTIAEEGFRGLMGKTSFNVARNALVN 180
OY 189 AAYGIVDTAK-----GMLPDPKNTFHVISMIAQVTVAVAGLTSVPFDTVRRMMQOS 242
DB 181 CAELVTYDLIKDALKANLMTDLPCHFTSAFGAGFCTTYVAS----PVDVYKTRYMNSA 236
OY 243 -GRKGTIMYTGTLDCWKRRIARDEGKAFFKGANSNVLK--GMGAFVLYLYDEIK 296
DB 237 LGQ-----YSSAGHCALTMLOKEGPRAFYKGFMPSPFLRLGSMVMVMEVTEYQLKR 286

```

```

RESULT 15
US-08-775-009-32
Sequence 32, Application US/08775009
Patent No. 5935783
GENERAL INFORMATION:
APPLICANT: Gong, Wellong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
Vellocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5935783rls, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:47:56 ; Search time 6.34043 Seconds
(without alignments)
677.670 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547

Sequence: 1 MTDAAISFAKDFLAGVAA.....LRMGAGVLYLYDEIKKYYT 298

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 92612 seqs, 14418503 residues

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubppa/PCCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppa/PCCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1547	100.0	298	10	US-09-811-094-32
2	1547	100.0	298	10	US-09-810-644-32
3	1454	94.0	298	10	US-09-811-094-33
4	1454	94.0	298	10	US-09-810-644-33
5	1391.5	89.9	297	10	US-09-811-094-31
6	1391.5	89.9	297	10	US-09-810-644-31
7	752.5	48.6	318	10	US-09-801-368-252
8	741.5	47.9	386	10	US-09-734-569-170
9	484	31.3	132	10	US-09-925-301-1459
10	484	29.0	87	10	US-09-864-761-38440
11	351	22.7	477	10	US-09-777-921A-2
12	350	22.6	475	10	US-09-777-921A-4
13	323.5	20.9	410	10	US-09-777-921A-5
14	302	19.5	469	9	US-09-992-598-289
15	302	19.5	469	10	US-09-989-722-289
16	302	19.5	469	10	US-09-988-723-289
17	302	19.5	469	10	US-09-989-729-289
18	302	19.5	469	10	US-09-989-727-289
19	302	19.5	469	10	US-09-989-731-289

20	302	19.5	469	10	US-09-989-732-289	Sequence 289, App
21	302	19.5	469	10	US-09-991-073-289	Sequence 289, App
22	302	19.5	469	10	US-09-990-442-289	Sequence 289, App
23	302	19.5	469	10	US-09-991-163-289	Sequence 289, App
24	302	19.5	469	10	US-09-993-604-289	Sequence 289, App
25	302	19.5	469	10	US-09-990-456-289	Sequence 289, App
26	302	19.5	469	10	US-09-989-721-289	Sequence 289, App
27	302	19.5	469	12	US-10-006-867-58	Sequence 58, App
28	297	19.2	342	10	US-09-777-921A-6	Sequence 6, App
29	261.5	16.9	289	10	US-09-796-766-20	Sequence 20, App
30	261	16.9	310	9	US-10-042-194-1	Sequence 1, App
31	252	16.3	131	10	US-09-925-300-1808	Sequence 1808, App
32	247	16.0	312	10	US-09-734-134-2	Sequence 2, App
33	247	16.0	312	10	US-09-826-507-2	Sequence 2, App
34	247	16.0	312	10	US-09-808-457-2	Sequence 2, App
35	246.5	15.9	309	10	US-09-884-814-8	Sequence 8, App
36	243.5	15.7	309	10	US-09-884-814-1	Sequence 1, App
37	239.5	15.5	309	10	US-09-884-814-6	Sequence 6, App
38	232	15.0	410	10	US-09-796-766-10	Sequence 10, App
39	230.5	14.9	320	10	US-09-840-787-12	Sequence 12, App
40	229	14.8	433	10	US-09-796-766-18	Sequence 18, App
41	227.5	14.7	275	10	US-09-808-457-4	Sequence 4, App
42	222.5	14.4	436	10	US-09-796-766-21	Sequence 21, App
43	221.5	14.3	323	12	US-10-006-867-126	Sequence 126, App
44	213.5	13.8	300	10	US-09-810-673A-6	Sequence 6, App
45	207	13.4	379	10	US-09-810-673A-4	Sequence 4, App

ALIGNMENTS

RESULT 1
US-09-811-094-32
; Sequence 32, Application US/09811094
; Patent No. US2001004144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Cleveenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yezhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT'),
; FILE REFERENCE: 660088, 420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-32

Query Match 100.0%; Score 1547; DB 10; Length 298;
Best local Similarity 100.0%; Pred. No. 3.6e-154;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGVAAIASTRVAPIERVLLLLQVHASKQITADKQKIIDCYVR 60
DB 1 MTDAAISFAKDFLAGVAAIASTRVAPIERVLLLLQVHASKQITADKQKIIDCYVR 60

QY 61 IPKEOEYLSWPKRNLNVIRFPFOALNFAFKYKQIFGVDKRTQFRYFAGNLASG 120
DB 61 IPKEOEYLSWPKRNLNVIRFPFOALNFAFKYKQIFGVDKRTQFRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARFLADVKGAGAEERFGIDGLVITYKSDGIKGLYGFNNV 180
DB 121 GAAGATSLCFVYPLDFARFLADVKGAGAEERFGIDGLVITYKSDGIKGLYGFNNV 180

Oy	181	VGGIIYVAAAFEGIYDPAKGLPBPKNTHIYISMIQOTYAVAGLSYEPDIYRRMM	24.0
Db	181	VGGIIYVAAAFGIYDPAKGLPBPKNTHIYISMIQOTYAVAGLSYEPDIYRRMM	24.0
Oy	241	QSGRGDYMNTGLDCCRKRTARDEGGAFFKGMASVNLKMGAFVLVLYDELRKKT	298
Db	241	QSGRGDYMNTGLDCCRRTARDEGGAFFKGMASVNLKMGAFVLVLYDELRKKT	298

RESULT 2

```

US-09-810-644-32
: Sequence 32, Application US/09810644
: Patent No. US20020012992A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Clevenger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Willer, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pei, Yanzhong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT)
: TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660088.42093
: CURRENT APPLICATION NUMBER: US/09/810,644
: CURRENT FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 32
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Homo sapien
US-09-810-644-32

```

Query Match	100.0%;	Score 1547;	DB 10;	Length 298;
Best Local Similarity	100.0%;	Pred. No. 3.6e-154;		
Matches 298;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	1	MTDAALSEAFDPLFAGVAAAIAKSTVAPERKILLLOVQASHKOTPDROKYOKEIIDCVBR	60
Db	1	MTDAALSEAFDPLFAGVAAAIAKSTVAPERKILLLOVQASHKOTPDROKYOKEIIDCVBR	60
Oy	61	IPKEQEVLSFWRCMLNVATREPTQALNFAEFKDKYQJIFLGVDKRTQFWRVEFAGNLASG	12
Db	61	IPKEQEVLSFWRCMLNVATREPTQALNFAEFKDKYQJIFLGVDKRTQFWRVEFAGNLASG	12
Oy	121	GAACTSLCFVYPLDAPRRLAADYDCKGAEKEFEFGJGDCVLYKESDGJIKGLYOGPNIS	18
Db	121	GAACTSLCFVYPLDAPRRLAADYDCKGAEKEFEFGJGDCVLYKESDGJIKGLYOGPNIS	18
Oy	181	VGGIIRAYAFSGIYDTAAGMLPDPKRNTHIVLSNMIAGTVAVAGLISYEPDFVRRMM	24
Db	181	VGGIIRAYAFSGIYDTAAGMLPDPKRNTHIVLSNMIAGTVAVAGLISYEPDFVRRMM	24
Oy	241	QSGKRGDVMYTGTLDCMKRIARDBGRAFFRGANSVNLBROMGAFVLVYIDELIKTYT	298
Db	241	QSGKRGDVMYTGTLDCMKRIARDBGRAFFRGANSVNLBROMGAFVLVYIDELIKTYT	298

RESULT 3

US-09-811-094-33
Sequence 33, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.

```

?   APPLICANT: Ghosh, Soumitra S.
?   APPLICANT: Moos, Walter H.
?   APPLICANT: Pel, Yezhong
?   TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
?   TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
?   FILE REFERENCE: 660088.42004
?   CURRENT APPLICATION NUMBER: US/09/811,094
?   CURRENT FILING DATE: 2001-03-14
?   NUMBER OF SEQ ID NOS: 37
?   SOFTWARE: FastSeq for Windows Version 3.0
?   SEQ ID NO 33
?   LENGTH: 298
?   TYPE: PRT
?   ORGANISM: Homo sapien
US-09-811-094-33

Query Match          94.0%; Score 1454; DB 10: Length 298;
Best Local Similarity 92.0%; Pctd. No. 1,9e+14;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps

```

US-09-811-094-33

[illegible]

RESULT 4
US-09-810-644-33
; Sequence 33, Application US/09810644
; Patent No. US20020012992A1

```

? GENERAL INFORMATION:
? APPLICANT: Anderson, Christen M.
? APPLICANT: Davis, Robert E.
? APPLICANT: Cleveneger, William
? APPLICANT: Wiley, Sandra Eileen
? APPLICANT: Wiliier, Scott W.
? APPLICANT: Szabo, Tomas R.
? APPLICANT: Ghosh, Soumitra S.
? APPLICANT: Moos, Walter H.
? APPLICANT: Pel, Yazhong
? TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT'),
? TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
? FILE REFERENCE: 660088.42003
? CURRENT APPLICATION NUMBER: US/09/810,644
? CURRENT FILING DATE: 2001-03-14
? NUMBER OF SEQ ID NOS: 37
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 33
? LENGTH: 298
? TYPE: PRT
? ORGANISM: Homo sapien
? US-09-810-644-33

```

Query Match

Best Local Similarity 92.68; Pred. No. 1,9e+14;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
1 MTDALSEKDFLAGVAAAIKSTAVAPLERVKLLIQVHASKQTADKQYGIIDCVR 60

RESULT 5
 US-09-811-094-31
 Sequence 31, Application US/09811094
 Patent No. US20010044144a1
 GENERAL INFORMATION:
 APPLICANT: Anderson, Christen M.
 APPLICANT: Davis, Robert E.
 APPLICANT: Clevenger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Waller, Scott W.
 APPLICANT: Szabo, Tomas R.
 APPLICANT: Ghosh, Soumitra S.
 APPLICANT: Moos, Walter H.
 APPLICANT: Pel, Yezhong
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (AMT)
 TITLE OF INVENTION: NOVEL AMT LIGANDS AND SCREENING ASSAYS THEREFOR
 FILE REFERENCE: 660088.4.20D4
 CURRENT APPLICATION NUMBER: US/09/811,094
 CURRENT FILING DATE: 2001-03-14
 NUMBER OF SEQ. ID NOS: 37
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ. ID NO 31
 LENGTH: 297
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-811-094-31

[illegible]

Query Match	89.9%	Score 1391.5	DB:10	Length 297
Best Local Similarity	88.6%	Pred. No. 6,4e-138		
Matches 263	Conservative 17	Mismatches 16	Indels 1	Gaps 1
Qy	1	MTDALSFADKDLAGGVAANAISKTAVAPIERVKLLQYOVHASKQITADKQYKGIIDCVVR	60	
Db	1	MDDHAMSFLEKDLAGVAANAASKTAVAPIERVKLLQYOVHASKQISAEKQYKGIIDCVVR	60	
Qy	61	IPKEDVLSFEMKGNLANVRYEPTQALNAPFDKXKQIFLGVVDKRTQWRFAPAGLWAG	120	
Db	61	IPKEDGFLSEFMKGNLANVRYEPTQALNAPFDKXKQIFLGVVDKRTQWRFAPAGLWAG	120	
Qy	121	GAAGATSLCEVYPLDFARTRLAADYGVKAGAEERFRLGDLVKYKXSDIKGLYOGFNVS	180	
Db	121	GAAGATSLCEVYPLDFARTRLAADYGVRR-AOREEFHGLDCCIIFKFSDDLGLGLYOGFNVS	179	
Qy	181	VGGIITVYRAAYGIVDTAKGMLPDPKNTHIVISMMIAQVTVAVAGLTSVPFDVRRRRMM	240	
Db	180	VGGIITVYRAAYGIVDTAKGMLPDRKNTHIVISMMIAQVTVAVAGLTSVPFDVRRRRMM	239	
Qy	241	OSGRKGTIDMYTGLDCKWRKIARDEGGAFFKFGAMSNVLRGMGAFVLYLDEIKKY	297	
Db	240	OSGRGAGADIMYGTGVDCWKRIAKDEGAKFFKFGAMSNVLRGMGAFVLYLDEIKKY	296	

```

1 RESULT 7
2 US-09-801-368-252
3 ; Sequence 252, Application US/09801368
4 ; Patent No. US20020128250A1
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Busby, Robert
7 ; APPLICANT: Cali, Brian
8 ; APPLICANT: Hecht, Peter
9 ; APPLICANT: Holtzman, Doug
10 ; APPLICANT: Madden, Kevin
11 ; APPLICANT: Maxon, Mary
12 ; APPLICANT: Milne, Todd
13 ; APPLICANT: No. US20020128250A1man, Thea
14 ; APPLICANT: Royer, John
15 ; APPLICANT: Salama, Sofie
16 ; APPLICANT: Sherman, Amir
17 ; APPLICANT: Silva, Jeff
18 ; APPLICANT: Summers, Eric
19 TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungus
20 FILE REFERENCE: 109272.147
21 CURRENT APPLICATION NUMBER: US/09/801,368
22 CURRENT FILING DATE: 2001-03-07
23 ;
24 ;
25 ;
26 ;
27 ;
28 ;
29 ;
30 ;
31 ;
32 ;
33 ;
34 ;
35 ;
36 ;
37 ;
38 ;
39 ;
40 ;
41 ;
42 ;
43 ;
44 ;
45 ;
46 ;
47 ;
48 ;
49 ;
50 ;
51 ;
52 ;
53 ;
54 ;
55 ;
56 ;
57 ;
58 ;
59 ;
60 ;
61 ;
62 ;
63 ;
64 ;
65 ;
66 ;
67 ;
68 ;
69 ;
70 ;
71 ;
72 ;
73 ;
74 ;
75 ;
76 ;
77 ;
78 ;
79 ;
80 ;
81 ;
82 ;
83 ;
84 ;
85 ;
86 ;
87 ;
88 ;
89 ;
90 ;
91 ;
92 ;
93 ;
94 ;
95 ;
96 ;
97 ;
98 ;
99 ;
100 ;

```

;; PRIOR APPLICATION NUMBER: US 09/487,558
;; PRIOR FILING DATE: 2000-01-19
;; PRIOR APPLICATION NUMBER: US 60/160,587
;; PRIOR FILING DATE: 1999-10-20
;; NUMBER OF SEQ ID NOS: 440
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 252
;; LENGTH: 318
;; TYPE: PRT
;; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-252

Query Match 48.6%; Score 752.5; DB 10; Length 318;
Best Local Similarity 54.3%; Pred. No. 4,4e-71;
Matches 159; Conservative 40; Mismatches 85; Indels 9; Gaps 5;

QY 7 SPANDELAGVAAASKRAVAPIERVKLLQVQ--HASKQIADKQKIIICVAPREQ 65
DB 22 NPLIDFLMGVSAAVAKTAASPIERVKLLIONODEMLKQGLDRKYAGILDCFKRTATQ 81
QY 66 EVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFPAGNLASGAGA 125
DB 82 GVISFMRGNLANVIRYPTQALNFAFKDKIKAMF--GFKKEGKAKWFPAGNLASGAGA 139
QY 126 TSLCFVYPLDFARTRLAAD--VGKAGAREFRGIDCVIKYKSDGIKGLYQGFNVSVQ 183
DB 140 LSLFVYSLDYARTRLAADSSKKGARQFGLIDYVKTKLSQGVAGLYRGFLPSVYG 199
QY 184 IIVRAAFEGYIDTPAKG-MLPDPKNTHTVISMIAQTVTAAGLTSYFDPVRRRMMQ 242
DB 200 IIVRKGFLFGMDSLKPLLLTGSLEGSFLASFLGAVTTGASTCSTYPLDVRRRMMT 259
QY 243 GRKGTIDIMYGTLDCKWRKIARDGSKAFKAGMSNVLRGMAFVLYDEIK 295
DB 260 GQA---VAYDGAFLDCKRIVAAGVGLFKGCGANILRGVAGVISMVDQ 309

RESULT 8
US-09-734-569-170
;; Sequence 170, Application US/09734569
;; Patent No. US20020064816A1
;; GENERAL INFORMATION:
;; APPLICANT: Lerchl, Jens
;; APPLICANT: Renz, Andreas
;; APPLICANT: Ehrhardt, Thomas
;; APPLICANT: Reinhardt, Andreas
;; APPLICANT: Cirpus, Petra
;; APPLICANT: Bischoff, Friedrich
;; APPLICANT: Frank, Markus
;; APPLICANT: Freund, Annette
;; APPLICANT: Duwenig, Elke
;; APPLICANT: Schmidt, Ralf-Michael
;; APPLICANT: Reski, Ralf
;; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
;; TITLE OF INVENTION: in the synthesis of carbohydrates
;; FILE REFERENCE: BASF-NAE-133J-99-US
;; CURRENT APPLICATION NUMBER: US/09/734,569
;; CURRENT FILING DATE: 2001-05-24
;; PRIOR APPLICATION NUMBER: US 60/177,101
;; PRIOR FILING DATE: 1999-12-16
;; NUMBER OF SEQ ID NOS: 181
;; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
;; SEQ ID NO 170
;; LENGTH: 386
;; TYPE: PRT
;; ORGANISM: Physcomitrella patens
US-09-734-569-170

Query Match 47.9%; Score 741.5; DB 10; Length 386;
Best Local Similarity 53.4%; Pred. No. 8e-70;
Matches 157; Conservative 42; Mismatches 86; Indels 9; Gaps 5;

QY 7 SFAKDLAGVAAAIKTAVAPIERVKLLQVQ--HASKQIADKQKIIICVAPREQ 65

DB 84 SFMDFLMGVSAAVSKRAPIERVKLLIONODEMLKSGRLSHPYKIGCFESRTYKDE 143
QY 66 EVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFPAGNLASGAGA 125
DB 144 GMSLMRGNLANVIRYPTQALNFAFKDYKSL--GTRKDDGKWKFPAGNLASGAGA 202
QY 126 TSLCFVYPLDFARTRLAADV--GKAGAREFRGIDCVIKYKSDGIKGLYQGFNVSVQ 182
DB 203 LSLFVYSLDYARTRLAADSSKKGGERQFNLGVYKTKLTNDGJAGLYRGFLPSVYG 262
QY 183 IIVRAAFEGYIDTPAKG-MLPDPKNTHTVISMIAQTVTAAGLTSYFDPVRRRMMQ 241
DB 263 GIIYRGLYFGIYDLSKRVVLGNLEGNFLASFLGMDITIGAGIASYPIDVRRRMMT 322
QY 242 SGRKGTIDIMYGTLDCKWRKIARDGSKAFKAGMSNVLRGMAFVLYDEIK 295
DB 323 SGEA---VKYNGSMDAFKQILLAKGASLFGAGANILRAVAGVLSGTDQ 373

RESULT 9
US-09-925-301-1459
;; Sequence 1459, Application US/09925301
;; Patent No. US20020052308A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;; FILE REFERENCE: PA106
;; CURRENT APPLICATION NUMBER: US/09/925,301
;; PRIOR FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: PCT/US00/05882
;; PRIOR FILING DATE: 2000-03-08
;; PRIOR APPLICATION NUMBER: 60/124,270
;; PRIOR FILING DATE: 1999-03-12
;; NUMBER OF SEQ ID NOS: 1694
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1459
;; LENGTH: 132
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (115)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (123)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (126)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (129)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1459

Query Match 31.3%; Score 484; DB 10; Length 132;
Best Local Similarity 87.9%; Pred. No. 1.5e-43;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDALSFAPKFLAGVAAAIKTAVAPIERVKLLQVQHSKQIADKQKIIICVAPREQ 60
DB 26 MTEQAISFAPKFLAGVAAAIKTAVAPIERVKLLQVQHSKQIADKQKIIICVAPREQ 85
QY 61 IPKQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRT 107
DB 86 IPKQGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRT 132

RESULT 10
US-09-864-761-36440
;; Sequence 36440, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aegomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36440
LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO L78810.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 6.00e-38
OTHER INFORMATION: EST_HUMAN HIT: AW935235.1, EVALUE 5.00e-37
US-09-864-761-36440

Query Match 29.0%; Score 448; DB 10; Length 87;
Best Local Similarity 100.0%; Pred. NO. 5.1e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
113 FAGNLASGAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGDLVKIYKSDGIKG 172
|||||

Db 1 FAGNLASGAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGDLVKIYKSDGIKG 60
Qy 173 LYGFNFNSVGCITTYRAAYFGIYDTAK 199
Db 61 LYGFNFNSVGCITTYRAAYFGIYDTAK 87

RESULT 11
US-09-777-921A-2
Sequence 2, Application US/09777921A
Patent No. US20020115136A1
GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: CLO01103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 477
TYPE: PRT
ORGANISM: Homo sapiens
US-09-777-921A-2

Query Match 22.7%; Score 351; DB 10; Length 477;
Best Local Similarity 31.5%; Pred. No. 7e-29;
Matches 93; Conservative 61; Mismatches 113; Indels 28; Gaps 10;
Qy 10 KDEFLAGVAAAIKSTAAPIERVLLQOVHASKQITADKRYKGIIDCVNIPREOEVL 69
Db 196 ROLLAGGIAGAVSRTSAPLRLKIMQV-HGSK--SDKM-NIFGFRQVREGGIRS 249
Qy 70 FMRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFRRYFAGNLASGAAGATSLC 129
Db 250 LMRNGTIVITAPETAVKFAFYEQYKLLTEEOQKICTFFRFTSGSR----AGATROT 304
Qy 130 FVYPLDFARTRLAADVKGAGAREFRGLGDLVKIYKSDGIKGLYGFNFNSVGCITTYRA 189
Db 305 FIYPMEVAKTRLA--VGKTG--OYSGIYDCAKKILKHEGIGAGFYKGVPMILGITPYAG 359
Qy 190 AVEGIDYDAK-----GMLPDPKNTIYVSMIAQTVTAVALGTSPPTFVRRMMOSGR 244
Db 360 IDLAVELKLSYWLDFRAKDSVNPVWVLGCGLASTCGOLASTPLALVTRMQAQAML 419
Qy 245 KGTDIMYGTLDCKWRIARDEGKAFKFGAMSN--VLRGAGAFVLYDEIKK 296
Db 420 EGSFQL--NMVGLFRRTISKIGIGLYRGITPMPKVLPAVGISY--VYENMQ 470

RESULT 12
US-09-777-921A-4
Sequence 4, Application US/09777921A
Patent No. US20020115136A1
GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: CLO01103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 475
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-777-921A-4

Query Match 22.6%; Score 350; DB 10; Length 475;
113 FAGNLASGAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGDLVKIYKSDGIKG 172
|||||

Best Local Similarity 31.2%; Pred. No. 8.9e-29;
Matches 92; Conservative 59; Mismatches 114; Indels 30; Gaps 9;
QY 10 KDLFAGVAAAIKSTAVAPLIERVKKLLQVHASKQITADKQYKGIIDCVVRIPKQEVLS 69
Db 196 ROLLGGTAVGASVRSSTAPLDRLKIMQV-HGSKM--NIFGGRQWKEGIRS 247
QY 70 FWRGNLAVIRFPTQALNFAFKDKYKQIFLGVDKRTQFWRVFAGNLASGAGATSLC 129
Db 248 LMRGCTGVIRKAPETAVKFMWYEQYKLLTEEGKIGTFEERFISGS-AGATAGT 302
QY 130 FVYPLDFARTLADYKAGAEERFRLGDLVKYKSDGKLGKYGFNVSQGIITIRRA 189
Db 303 FLYPMWAKTRILA-VGKRG--QYSGIYDCAKKILKEGFGAFKGYVPMNLGITIPYAG 357
QY 190 AVFGIYDRAK-----GMLPDKNTHIVISMIAQVTVAVAGLTSVPPTVRRRMQSGR 244
Db 358 IDLAVYELKSHMDNFAKDSVNPGLVLLGCGALSTCGOLASTYPLALVTRMQAQL 417
QY 245 KCTDIYMTGLDWCRRKIRARDEGKAFKAGMSN--VLKMGCAFVLVLYDEIKR 296
Db 418 ECAQPL--NMVGLFRRIISKEQLPGLYRGITPNEKVLPAVGISY--VYENMKQ 468

RESULT 13
US-09-777-921A-5
; Sequence 5, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CLE001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921A-5

Query Match 20.9%; Score 323.5; DB 10; Length 410;
Best Local Similarity 33.6%; Pred. No. 4.3e-26;
Matches 80; Conservative 46; Mismatches 91; Indels 21; Gaps 7;
QY 10 KDLFAGVAAAIKSTAVAPLIERVKKLLQVHASKQITADKQYKGIIDCVVRIPKQEVLS 69
Db 189 ROLLGGTAVGASVRSSTAPLDRLKIMQV-HGSKM--NIFGGRQWKEGIRS 242
QY 70 FWRGNLAVIRFPTQALNFAFKDKYKQIFLGVDKRTQFWRVFAGNLASGAGATSLC 129
Db 243 LMRGCTGVIRKAPETAVKFMWYEQYKLLTEEGKIGTFEERFISGS-AGATAGT 297
QY 130 FVYPLDFARTLADYKAGAEERFRLGDLVKYKSDGKLGKYGFNVSQGIITIRRA 189
Db 298 FLYPMWAKTRILA-VGKRG--QYSGIYDCAKKILKEGFGAFKGYVPMNLGITIPYAG 352
QY 190 AVFGIYDRAK-----GMLPDKNTHIVISMIAQVTVAVAGLTSVPPTVRRRMQSGR 242
Db 353 IDLAVYELKSHMDNFAKDSVNPGLVLLGCGALSTCGOLASTYPLALVTRMQAQL 410

RESULT 14
US-09-992-598-289
; Sequence 289, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202

```

1 PRIOR APPLICATION NUMBER: 60/090444
2 PRIOR FILING DATE: 1998-06-24
3 PRIOR APPLICATION NUMBER: 60/090445
4 PRIOR FILING DATE: 1998-06-24
5 PRIOR APPLICATION NUMBER: 60/090472
6 PRIOR FILING DATE: 1998-06-24
7 PRIOR APPLICATION NUMBER: 60/090535
8 PRIOR FILING DATE: 1998-06-24
9 PRIOR APPLICATION NUMBER: 60/090540
10 PRIOR FILING DATE: 1998-06-24
11 PRIOR APPLICATION NUMBER: 60/090542
12 PRIOR FILING DATE: 1998-06-24
13 PRIOR APPLICATION NUMBER: 60/090557
14 PRIOR FILING DATE: 1998-06-24
15 PRIOR APPLICATION NUMBER: 60/090676
16 PRIOR FILING DATE: 1998-06-25
17 PRIOR APPLICATION NUMBER: 60/090678
18 PRIOR FILING DATE: 1998-06-25
19 PRIOR APPLICATION NUMBER: 60/090690
20 PRIOR FILING DATE: 1998-06-25
21 PRIOR APPLICATION NUMBER: 60/090694
22 PRIOR FILING DATE: 1998-06-25
23 PRIOR APPLICATION NUMBER: 60/090695
24 PRIOR FILING DATE: 1998-06-25
25 PRIOR APPLICATION NUMBER: 60/090696
26 PRIOR FILING DATE: 1998-06-25
27 PRIOR APPLICATION NUMBER: 60/090862
28 PRIOR FILING DATE: 1998-06-26
29 PRIOR APPLICATION NUMBER: 60/090863
30 PRIOR FILING DATE: 1998-06-26
31 PRIOR APPLICATION NUMBER: 60/091360
32 PRIOR FILING DATE: 1998-07-01
33 PRIOR APPLICATION NUMBER: 60/091478
34 PRIOR FILING DATE: 1998-07-02
35 PRIOR APPLICATION NUMBER: 60/091544
36 PRIOR FILING DATE: 1998-07-01
37 PRIOR APPLICATION NUMBER: 60/091519
38 PRIOR FILING DATE: 1998-07-02
39 PRIOR APPLICATION NUMBER: 60/091626
40 PRIOR FILING DATE: 1998-07-02
41 PRIOR APPLICATION NUMBER: 60/091633
42 PRIOR FILING DATE: 1998-07-02
43 PRIOR APPLICATION NUMBER: 60/091978
44 PRIOR FILING DATE: 1998-07-07
45 PRIOR APPLICATION NUMBER: 60/091982
46 PRIOR FILING DATE: 1998-07-07
47 PRIOR APPLICATION NUMBER: 60/092182
48 PRIOR FILING DATE: 1998-07-09
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
85
```

RESULT 15
US-09-989-722-289
Sequence 289, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349

```
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
```

Query Match 19.5%; Score 302; DB 10; Length 469;
Best Local Similarity 29.1%; Pred. No. 9.1e-24;
Matches 86; Conservative 60; Mismatches 118; Indels 32; Gaps 11;

```
OY 10 KDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKGIIDCVRIPEQOEYLS 69
Db 188 RHLVAGGAGAVSTRCTAPDRLKVLMOY-HASR-----SNMGIVGFTOMIREGARS 241
OY 70 FWRGNLANVIRYPTOLNFAFKDKYKOIFIGVDKRTQFWRYPAGNLAGSAGAGATSLC 129
Db 242 LMRNGNINVLKIAPESAIKFMAYEQIKR--LVGSDQET---LRIHERLVAGSLAGATAQS 296
OY 130 FVYPLDFARTRLADVGKAGAEFRGLGDCLVKIKYKSDGIKGLYOGFNVSVOGIITRYA 189
Db 297 SIYMEVLKTRMA--LKRKTG---QYSGMLDCARILAREGVAAFYKGVVPMILGIIPYAG 351
```

```
OY 190 AVEGIYDTAKM-----LPDPKNTHIVISMIAQTVTAVAG-LTSYPEDTVRRMM 240
Db 352 IDLAVYETLKNAMLOHYAVNSADPG---VFVLLACGTMSSTCQLASYPLALVTRMOA 407
OY 241 QSGRKGTDIMYTGTLDCWRKILARDEGGAFFKGAWSNVLRGMGAFV-LVLYDEIK 295
Db 408 QASIEGAPEVTMSSL--FKHILRTGAFGLYRGLAPNFMKVIYPAVSISYVENLK 461
```

Search completed: November 12, 2002, 16:56:56
Job time : 7.34043 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:05 : Search time 14.0157 Seconds

(without alignments)
2044.001 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547
Sequence: 1 MTDALSFADFLAGGVAAA.....LRGMGCAFVLVLEIKKKT 298Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

PIR 73: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	1 A29132	ADP, ATP carrier pr
2	1479	95.6	298	2 S31814	ADP, ATP carrier pr
3	1458	94.2	298	2 B43646	ADP, ATP carrier pr
4	1454	94.0	298	1 S03894	ADP, ATP carrier pr
5	1419	91.7	298	1 XMBO	ADP, ATP carrier pr
6	1417	91.6	298	2 S37210	ADP, ATP carrier pr
7	1417	91.6	298	2 T60173	adenine nucleotide
8	1413	91.3	298	1 A44778	ADP, ATP carrier pr
9	1110	75.6	300	1 S31935	ADP, ATP carrier pr
10	1032	66.7	300	2 T25371	hypothetical prote
11	1029	66.5	313	2 T23207	hypothetical prote
12	1029	66.5	313	2 T25850	hypothetical prote
13	986	63.7	300	2 T15206	hypothetical prote
14	986	62.6	339	2 A41677	ADP, ATP carrier pr
15	938	60.6	301	2 S51132	ADP, ATP carrier pr
16	771	49.8	386	2 T09709	ADP, ATP carrier pr
17	770	49.8	322	2 T40526	adp/atp translocas
18	765	49.5	308	1 S30259	ADP, ATP carrier pr
19	761.5	49.2	307	2 A36582	ADP, ATP carrier pr
20	759	49.1	326	2 T25728	hypothetical prote
21	759	49.1	367	2 S14876	ADP, ATP carrier pr
22	757	48.9	313	1 XMNC	ADP, ATP carrier pr
23	754	48.7	386	2 S17917	ADP, ATP carrier pr
24	753	48.7	387	2 S16568	ADP, ATP carrier pr
25	752.5	48.6	318	1 A31978	ADP, ATP carrier pr
26	752	48.6	386	2 S21974	ADP, ATP carrier pr
27	749.5	48.4	305	2 S68154	ADP, ATP carrier pr
28	749.5	48.4	306	2 T20012	hypothetical prote
29	746	48.2	306	2 T42011	ADP, ATP carrier pr

30	746	48.2	379	2 T04608	ADP, ATP carrier pr
31	745.5	48.2	385	1 S29852	ADP, ATP carrier pr
32	745	48.2	382	2 S33630	ADP, ATP carrier pr
33	741.5	47.9	379	2 S21313	ADP, ATP carrier pr
34	741.5	47.9	386	2 S14874	ADP, ATP carrier pr
35	728	47.1	309	2 A24849	ADP, ATP carrier pr
36	665.5	43.0	298	2 T24029	hypothetical prote
37	521.5	33.7	327	2 T51577	ADP, ATP translocas
38	388	25.1	325	2 T04273	hypothetical prote
39	372	24.0	381	2 T51158	hypothetical prote
40	372	24.0	415	2 T48171	hypothetical prote
41	356	23.0	352	2 T01729	mitochondrial solu
42	350	22.6	475	2 T50686	peroxisomal Ca-dep
43	340	22.0	358	2 T45934	hypothetical prote
44	334	21.6	348	2 D84798	probable mitochond
45	322.5	20.8	332	2 T47703	Ca-dependent solut

ALIGNMENTS

```
RESULT 1
ADP, ATP carrier protein T2 - human
A: Accession: A29132
N: Alternate names: mitochondrial ADP, ATP translocase 2
C: Species: Homo sapiens (man)
C: Date: 17-Mar-2000 #Sequence_Revision 17-Mar-2000 #text_change 17-Mar-2000
C: Accession: A29132; C28116
R: Batini, R.; Ferrarini, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
J. Biol. Chem. 262, 4355-4359, 1987
A: Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regi
A: Reference number: A29132; MIMID:8716056; PMID:3031073
A: Accession: A29132
A: Molecule type: mRNA
A: Residues: 1-298 <BAT>
A: Cross-references: GB:J02683; NID:q179246; PIDD:AAA35579.1; PID:q179247
R: Houldsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A: Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A: Reference number: A94197; MIMID:88124845; PMID:2829183
A: Molecule type: mRNA
A: Residues: 47-65 'G', 67-110 'L', 112-161 'G', 163-298 <HOU>
A: Cross-references: GB:J03591; NID:q339720; PIDD:AAA36749.1; PID:q339721
A: Experimental source: Clone PHAT3
C: Genetics:
A: Gene: GDB:ANT2; T3; 2P1
A: Cross-references: GDB:125190; OMIM:300150
A: Map position: Xq13-Xq26
A: Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
C: Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C: Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F: 5-99/Domain: ADP, ATP carrier protein repeat homology <ACPI>
F: 110-202/Domain: ADP, ATP carrier protein repeat homology <ACPI>
F: 207-298/Domain: ADP, ATP carrier protein repeat homology <ACPI>
```

Query Match 100.0%; Score 1547; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 3.8e-130;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSFADFLAGGVAAAISKRAVAPTRVKLLLOVHASKOITTDKQYKGIIDCVVR 60
Db 1 MTDALSFADFLAGGVAAAISKRAVAPTRVKLLLOVHASKOITTDKQYKGIIDCVVR 60

QY 61 IPKEQEVLSFMKGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
Db 61 IPKEQEVLSFMKGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDPAKTLADAVCAKAGAEERERGLGDCLVKTKYKSDGKIGLYOGFNVS 180
Db 121 GAAGATSLCFVYPLDPAKTLADAVCAKAGAEERERGLGDCLVKTKYKSDGKIGLYOGFNVS 180

QY 181 VQGIITRAVYFGIYDPAKMLDPKKNTHLVISWMLAQVTAVAGLSYFDFVRRRMM 240

```

Db 181 VGGIIIRAAAFGIYDPAKGMIPDPKNTHTVISMIAQTAVAVAGLTSYPEDTVRRMM 240
QY 241 QSGRRGTDIMVTGLDCWKRITARDEGKAFFKGAMSNVLRMGAFVLYLYDELTKKYT 298
Db 241 QSGRRGTDIMVTGLDCWKRITARDEGKAFFKGAMSNVLRMGAFVLYLYDELTKKYT 298

RESULT 2
S31814
ADP, ATP carrier protein T2 - mouse
N:Alternate names: adenine nucleotide translocase
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
C:Accession: S31814
R:Costet, P.; Laplace, C.
submitted to the EMBL data library, January 1993
A:Reference number: S31814
A:Accession: S31814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <COS>
A:Cross-references: EMBL:X70847
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 95.6%; Score 1479; DB 2; Length 298;
Best Local Similarity 95.6%; Pred. No. 4,3e-124;
Matches 285; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAIASTKAVAPIERVKLLQVHASKOITADKOYGIIDCVR 60
Db 1 MTDALSPAKDFLAGVAAIASTKAVAPIERVKLLQVHASKOITADKOYGIIDCVR 60
QY 61 IPKEOVLSEFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
Db 61 IPKEOVLSEFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFEYPLDPFARTRIADVGKASGERERGLDCLVTKSDGIRGLYQGFNV 180
Db 121 GAAGATSLCFEYPLDPFARTRIADVGKASGERERGLDCLVTKSDGIRGLYQGFNV 180
QY 181 VGGIIIRAAAFGIYDPAKGMIPDPKNTHTVISMIAQTAVAVAGLTSYPEDTVRRMM 240
Db 181 VGGIIIRAAAFGIYDPAKGMIPDPKNTHTVISMIAQTAVAVAGLTSYPEDTVRRMM 240
QY 241 QSGRRGTDIMVTGLDCWKRITARDEGKAFFKGAMSNVLRMGAFVLYLYDELTKKYT 298
Db 241 QSGRRGTDIMVTGLDCWKRITARDEGKAFFKGAMSNVLRMGAFVLYLYDELTKKYT 298

RESULT 3
B43646
ADP,ATP carrier protein T2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
C:Accession: B43646
R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A:Reference number: A43646; MUID:8922093; PMID:2540808
A:Accession: B43646
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <POM>
A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>

```

```

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1458; DB 2; Length 298;
Best Local Similarity 92.9%; Pred. No. 3,2e-122;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAIASTKAVAPIERVKLLQVHASKOITADKOYGIIDCVR 60
Db 1 MTDALSPAKDFLAGVAAIASTKAVAPIERVKLLQVHASKOITADKOYGIIDCVR 60
QY 61 IPKEOVLSEFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
Db 61 IPKEOVLSEFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFEYPLDPFARTRIADVGKASGERERGLDCLVTKSDGIRGLYQGFNV 180
Db 121 GAAGATSLCFEYPLDPFARTRIADVGKASGERERGLDCLVTKSDGIRGLYQGFNV 180
QY 181 VGGIIIRAAAFGIYDPAKGMIPDPKNTHTVISMIAQTAVAVAGLTSYPEDTVRRMM 240
Db 181 VGGIIIRAAAFGIYDPAKGMIPDPKNTHTVISMIAQTAVAVAGLTSYPEDTVRRMM 240
QY 241 QSGRRGTDIMVTGLDCWKRITARDEGKAFFKGAMSNVLRMGAFVLYLYDELTK 296
Db 241 QSGRRGTDIMVTGLDCWKRITARDEGKAFFKGAMSNVLRMGAFVLYLYDELTK 296

RESULT 4
S03894
ADP,ATP carrier protein T3 - human
N:Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: S03894; B28116
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:89236396; PMID:2541251
A:Accession: S03894
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <COZ>
R:Houldsworth, J.; Altard, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:88124845; PMID:2829183
A:Accession: B28116
A:Molecule type: mRNA
A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
A:Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT3; ANT3Y
A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.0%; Score 1454; DB 1; Length 298;
Best Local Similarity 92.6%; Pred. No. 7,3e-122;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAIASTKAVAPIERVKLLQVHASKOITADKOYGIIDCVR 60
Db 1 MTDALSPAKDFLAGVAAIASTKAVAPIERVKLLQVHASKOITADKOYGIIDCVR 60
QY 61 IPKEOVLSEFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
Db 61 IPKEOVLSEFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120

```

Db 61 IPKDEGLSEFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRNQFWRYFAGNLSG 120
 QY 121 GAAGATSLCFYPPIDFARTRIADVGKAGARERERGLDCLVTKYKSDGKGLYOGFNV 180
 Db 121 GAAGATSLCFYPPIDFARTRIADVGKAGARERERGLDCLVTKYKSDGKGLYOGFNV 180
 QY 181 VGGIITIRAAAFGVYDPAKGMPLPDKNTHIVSMIAOTVAVAGLVSYPEDTVRRRMM 240
 Db 181 VGGIITIRAAAFGVYDPAKGMPLPDKNTHIVSMIAOTVAVAGLVSYPEDTVRRRMM 240
 QY 241 QSGRRKGDIMYTGTLDCWRKIARDEGKAFFKAGMSNVLRMGAFVLYLDEIKK 296
 Db 241 QSGRRKGDIMYTGTLDCWRKIARDEGKAFFKAGMSNVLRMGAFVLYLDEIKK 296

RESULT 5

XMBO
 ADP/ATP carrier protein T1 - bovine
 N:Alternate names: ADP/ATP translocase T1
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A43646; A24822; A03181; A61343; S69369
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A>Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: A43646
 A:Molecule type: mRNA
 A:Residues: 1-298 <PDM>
 A:Cross-references: GB:M24102; NID:g529414; PID:AAA30768.1; PID:g529415
 R:Rasmussen, U.B.; Mohlrah, H.
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986
 A>Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
 A:Reference number: A24822; MUID:8629575; PMID:3017341
 A:Accession: A24822
 A:Molecule type: mRNA
 A:Residues: 208-298 <RAS>
 A:Cross-references: GB:M13783; NID:g162630; PID:AAA30363.1; PID:g162631
 R:Aquila, H.; Misra, D.; Eulitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 343-349, 1982
 A>Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A03181; MUID:82188267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: protein
 A:Residues: 251, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AQU>
 A:Note: residue 52 may be methyllysine
 R:Abdel, W.; Wächter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A>Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A61343; MUID:82046808; PMID:6271240
 A:Accession: A61343
 A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oetmeier, W.; Masson, K.; Kallina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A>Title: [(3)H]-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
 A:Reference number: S69369; MUID:55172050; PMID:7867632
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63,154-168 <OET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A:Note: Located in the inner mitochondrial membrane
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 91.7%; Score 1419; DB 1; Length 298;
 Best Local Similarity 89.9%; Pred. No. 9.5e-119;
 Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDALSFPAKDLFAGVAAIASTKTAAPVIERVKLLQVHASKOITADKQYKGIIDCV 60
 Db 1 MSDALSFPAKDLFAGVAAIASTKTAAPVIERVKLLQVHASKOITADKQYKGIIDCV 60
 QY 61 IPKDEVLSEFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRNQFWRYFAGNLSG 120
 Db 61 IPKDEVLSEFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRNQFWRYFAGNLSG 120
 QY 121 GAAGATSLCFYPPIDFARTRIADVGKAGARERERGLDCLVTKYKSDGKGLYOGFNV 180
 Db 121 GAAGATSLCFYPPIDFARTRIADVGKAGARERERGLDCLVTKYKSDGKGLYOGFNV 180
 QY 181 VGGIITIRAAAFGVYDPAKGMPLPDKNTHIVSMIAOTVAVAGLVSYPEDTVRRRMM 240
 Db 181 VGGIITIRAAAFGVYDPAKGMPLPDKNTHIVSMIAOTVAVAGLVSYPEDTVRRRMM 240
 QY 241 QSGRRKGDIMYTGTLDCWRKIARDEGKAFFKAGMSNVLRMGAFVLYLDEIKK 297
 Db 241 QSGRRKGDIMYTGTLDCWRKIARDEGKAFFKAGMSNVLRMGAFVLYLDEIKK 297

RESULT 6

S37210
 ADP/ATP carrier protein T1 - mouse
 N:Alternate names: adenine nucleotide carrier
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S37210
 R:Laplace, C.; Costet, P.
 submitted to the EMBL Data Library, September 1993
 A:Reference number: S37210
 A:Accession: S37210
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <LAP>
 A:Cross-references: EMBL:X74510; NID:g402627; PID:CAA52616.1; PID:g402628
 C:Genetics:
 A:Gene: ANCL
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 91.6%; Score 1417; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1.4e-118;
 Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDALSFPAKDLFAGVAAIASTKTAAPVIERVKLLQVHASKOITADKQYKGIIDCV 60
 Db 1 MGDALSFPAKDLFAGVAAIASTKTAAPVIERVKLLQVHASKOITADKQYKGIIDCV 60
 QY 61 IPKDEVLSEFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRNQFWRYFAGNLSG 120
 Db 61 IPKDEVLSEFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRNQFWRYFAGNLSG 120
 QY 121 GAAGATSLCFYPPIDFARTRIADVGKAGARERERGLDCLVTKYKSDGKGLYOGFNV 180
 Db 121 GAAGATSLCFYPPIDFARTRIADVGKAGARERERGLDCLVTKYKSDGKGLYOGFNV 180
 QY 181 VGGIITIRAAAFGVYDPAKGMPLPDKNTHIVSMIAOTVAVAGLVSYPEDTVRRRMM 240
 Db 181 VGGIITIRAAAFGVYDPAKGMPLPDKNTHIVSMIAOTVAVAGLVSYPEDTVRRRMM 240
 QY 241 QSGRRKGDIMYTGTLDCWRKIARDEGKAFFKAGMSNVLRMGAFVLYLDEIKK 297
 Db 241 QSGRRKGDIMYTGTLDCWRKIARDEGKAFFKAGMSNVLRMGAFVLYLDEIKK 297

```
RESULT 7
160173
adenine nucleotide translocator - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: 160173
R:Shinozuka, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
B:Biochim. Biophys. Acta 1152, 192-196, 1993
A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat
A:Reference number: 160173; MUID:94002161; PMID:8399300
A:Accession: 160173
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-298 <RES>
A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
C:Genetics:
A:Gene: anti
A:Introns: 37/3; 200/1; 247/1
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match          91.6%; Score 1417; DB 2; Length 298;
Best Local Similarity 89.6%; Pred. No. 1.4e-118;
Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTDALSFKDFLAGVAAAIKSTAVAPLERKLLQVHASKQITADKQYGIIDCYVR 60
DB 1 MGDQALSFKDFLAGVAAAVKSTAVAPLERKLLQVHASKQISAEKQYGIIDCYVR 60
QY 61 IRKEQEVLSFWMGNLANVRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFAAGNLASG 120
DB 61 IRKEQGFSLFWMGNLANVRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFAAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGKAGAEERFGLGDCLVKIKYSDIKGLYOGFNV 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGAEERFGLGDCLVKIKYSDIKGLYOGFNV 180
QY 181 VGGIITRYRAYFGYDTAKGMLPDPKNTHTIVSMIAQVTVAGLTSVPPTVRRRMM 240
DB 181 VGGIITRYRAYFGYDTAKGMLPDPKNTHTIVSMIAQVTVAGLTSVPPTVRRRMM 240
QY 241 QSGRKGTIDIMYGTLDQWCKRIARDEGKAFFGAGSNVLRGNGAFVLYLDEIKKY 297
DB 241 QSGRKGTIDIMYGTLDQWCKRIARDEGKAFFGAGSNVLRGNGAFVLYLDEIKKY 297

RESULT 8
A44778
ADP,ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP,ATP translocase 1
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: A44778; S03893; A39891; A28116
R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.
J. Biol. Chem. 264, 13998-14004, 1999
A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A:Reference number: A44778; MUID:89340499; PMID:2547778
A:Accession: A44778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LIA>
A:Cross-references: GB:J04982; NID:9178658; PIDN:AAA51736.1; PID:9178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
A:Reference number: S03893; MUID:89236396; PMID:2541251
A:Accession: S03893
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <COZ>
```

```
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a lea
A:Reference number: A39891; MUID:86041149; PMID:2823266
A:Accession: A39891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A',17-146, 'RR',149,151-226, 'L',228-298 <NEC>
A:Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920
A:Experimental source: clone PHMAN1
R:Houldsworth, J.; Attardi, G. 85, 377-381, 1988
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level i
A:Reference number: A94197; MUID:86124845; PMID:2829183
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOU>
A:Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT1; T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match          91.3%; Score 1413; DB 1; Length 298;
Best Local Similarity 89.2%; Pred. No. 3.3e-118;
Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDALSFKDFLAGVAAAIKSTAVAPLERKLLQVHASKQITADKQYGIIDCYVR 60
DB 1 MGDHMSFLKDFLAGVAAAVKSTAVAPLERKLLQVHASKQISAEKQYGIIDCYVR 60
QY 61 IRKEQEVLSFWMGNLANVRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFAAGNLASG 120
DB 61 IRKEQGFSLFWMGNLANVRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFAAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGKAGAEERFGLGDCLVKIKYSDIKGLYOGFNV 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGAEERFGLGDCLVKIKYSDIKGLYOGFNV 180
QY 181 VGGIITRYRAYFGYDTAKGMLPDPKNTHTIVSMIAQVTVAGLTSVPPTVRRRMM 240
DB 181 VGGIITRYRAYFGYDTAKGMLPDPKNTHTIVSMIAQVTVAGLTSVPPTVRRRMM 240
QY 241 QSGRKGTIDIMYGTLDQWCKRIARDEGKAFFGAGSNVLRGNGAFVLYLDEIKKY 297
DB 241 QSGRKGTIDIMYGTLDQWCKRIARDEGKAFFGAGSNVLRGNGAFVLYLDEIKKY 297

RESULT 9
S31935
ADP,ATP carrier protein - African malaria mosquito
C:Species: Anopheles gambiae (African malaria mosquito)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S31935; S31936
R:Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
submitted to the EMBL Data Library, February 1993
A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
A:Reference number: S31935
A:Accession: S31935
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <BEA>
A:Cross-references: EMBL:Z21814; EMBL:Z21815
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>
```

DB 250 -DLVYKNTLDCAKKLIQNEGMSAMFKGALSNVERGTGALVLAIDELQKF 299

yearly mean	00.00; score 1022; D5 2; Dengchun 215;
Best Local Similarity	70.88; Pred. No. 5.5e-84;
Matches 206; Conservative	28; Mismatches 53; Indels 4; Gaps 3;

Db 63 RVSKQGVLSLRGNVANVIRFPTQAFNFAKDYFNIF-PRYDQNTD3SKFECVNILS 121
Qy 120 GGAGATSLCFVYPLDFARTRLADVKGAGAREFRGLGDCLVKTKSDGKGLYQGFNV 179
Db 122 GATGATSLILYVPLDFARTRLASDIGN-KGDRQFTGLFDCLAKIKOT3LSTLYSGFGV 180
Qy 180 SVOGIIRAAVFGIYDFAKGM-L-PDPKNTHHVISMIAQVTAVAGLTSYPEDTVRRRM 238
Db 181 SVTGIIYRGSI FGLYDSAKALLFTNDKNTNIVLKMVAQSVTILAGLISYPEDTVRRRM 240
Qy 239 MMOSGRKG-TDIMYTGFLDCWRKILARDEGKAFFKGANSNVLKMGGAFLVLYDEIKK 296
Db 241 MMSGRKGKEIYKNTIDCWIKILRNKGFKGFGKAMANVIRGAGALVLYFVDELQK 299

Search completed: November 12, 2002, 16:48:37
Job time : 15.0157 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:20 ; Search time 7.67525 Seconds
(without alignments)
1610.364 Million cell updates/sec

Title: US-09-393-441-32
Perfect score: 1547

Sequence: 1 MTDALSFADFLAGVAAA.....LRMGAFVLVYDEIRKYY 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1537	99.4	298	ADT2_HUMAN	P05141 homo sapien
2	1525	98.6	298	ADT2_RAT	Q09073 rattus norv
3	1519	98.2	298	ADT2_MOUSE	P51881 mus musculu
4	1458	94.2	298	ADT3_BOVIN	P32007 bos taurus
5	1454	94.0	298	ADT3_HUMAN	P12236 homo sapien
6	1417	91.6	298	ADT1_MOUSE	P49562 mus musculu
7	1417	91.6	298	ADT1_RAT	Q05962 rattus norv
8	1414	91.4	297	ADT1_BOVIN	P02722 bos taurus
9	1413	91.3	298	ADT1_HUMAN	P12235 homo sapien
10	1218.5	76.8	297	ADT_DROME	Q26365 drosophila
11	1190	76.9	301	ADT_ANOGA	Q27238 anopheles g
12	968	62.6	339	ADT_CHLKE	P31692 chlorella k
13	771	49.8	386	ADT1_GOSHI	Q22342 gossypium h
14	770	49.8	322	ADT1_SCHPO	Q09188 schizosacch
15	765	49.5	308	ADT_CHLRE	P27080 chlamydomon
16	761.5	49.2	307	ADT3_YEAST	P18238 saccharomyc
17	759	49.1	387	ADT1_MAIZE	P04709 zea mays (m
18	757	48.9	313	ADT_NEUCR	P02723 neurospora
19	753.5	48.7	385	ADT2_ARATH	P40941 arabidopsis
20	753	48.7	387	ADT2_MAIZE	P1857 zea mays (m
21	752.5	48.6	318	ADT2_YEAST	P18239 saccharomyc
22	752	48.6	386	ADT1_SOLFU	P32691 solanum tub
23	750	48.5	382	ADT_ORYSA	P31691 oryza sativ
24	749.5	48.4	305	ADT_KUOLA	P43982 kluyveromyc
25	747.5	48.3	381	ADT1_ARATH	P31167 arabidopsis
26	744	48.1	331	ADT1_WHEAT	Q41629 triticum ae
27	741.5	47.9	386	ADT2_SOLFU	P27081 solanum tub
28	737	47.6	331	ADT2_WHEAT	Q41630 triticum ae
29	728	47.1	309	ADT1_YEAST	P04710 saccharomyc
30	307	19.8	588	CMC2_CAEEL	Q20799 caenorhabdi
31	302	19.5	587	CMC3_CAEEL	Q19529 caenorhabdi
32	285	18.4	330	GDC_BOVIN	Q01888 bos taurus
33	284	18.4	307	ODC2_YEAST	Q09297 saccharomyc

34	278	18.0	325	1	UCP5_MOUSE	Q92822 mus musculu
35	276.5	17.9	322	1	GDC_RAT	P16261 rattus norv
36	276.5	17.9	702	1	CMC1_CAEEL	Q21153 caenorhabdi
37	276	17.8	678	1	CMC1_HUMAN	Q75746 homo sapien
38	274	17.7	325	1	UCP5_HUMAN	Q95258 homo sapien
39	265.5	17.2	332	1	GDC_HUMAN	P16260 homo sapien
40	261.5	16.9	675	1	CMC2_HUMAN	Q91560 homo sapien
41	261	16.9	310	1	ODC1_YEAST	Q03028 saccharomyc
42	257.5	16.6	315	1	MTF_HUMAN	Q91261 homo sapien
43	249.5	16.1	326	1	YE08_SCHPO	Q13805 schizosacch
44	249	16.1	315	1	SA18_HUMAN	Q91144 homo sapien
45	249	16.1	324	1	ODC1_YEAST	P32332 saccharomyc

ALIGNMENTS

RESULT 1
ADT2_HUMAN
ID ADT2_HUMAN STANDARD: PRT: 298 AA.
AC P05141: 043350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
CN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Murzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
BA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraia R.,
MA Mazzarella R.A., Schlessinger D., Chen E.Y.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX Becker M., Graves T., Ozerky P.;
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houdsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
level in adult human liver."
RT Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -I- SUBUNIT: MONOMER.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: M57424; AAA51737.1; -
 DR EMBL: J02683; AAA35579.1; -
 DR EMBL: L78810; AAB39266.1; -
 DR EMBL: AC004000; AAB96347.1; -
 DR EMBL: J03591; AAA36749.1; -
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR Genew: HGNC:10991; SLC25A5.
 DR MIM: 300150; -
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr. 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 FT SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 99.4%; Score 1537; DB 1; Length 298;
 Best local Similarity 99.3%; Pred. No. 9.4e-130;
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTPAALSFADFLAGVAAAIKSTAVAPIERVKLLQVGHASKQTADKQYKGIIDCVR 60
 FT 1 MTPAALSFADFLAGVAAAIKSTAVAPIERVKLLQVGHASKQTADKQYKGIIDCVR 60
 DB 1 MTPAALSFADFLAGVAAAIKSTAVAPIERVKLLQVGHASKQTADKQYKGIIDCVR 60

QY 61 IPKEOVLSTFWRGNLANVIRYPTQALNFAFKYKQIFLGVDKRTQFWRYPAGNLASG 120
 FT 61 IPKEOVLSTFWRGNLANVIRYPTQALNFAFKYKQIFLGVDKRTQFWRYPAGNLASG 120
 DB 61 IPKEOVLSTFWRGNLANVIRYPTQALNFAFKYKQIFLGVDKRTQFWRYPAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRLADVKGAGAEERFGLGDLVYKSDGKGLYQGFNVS 180
 FT 121 GAAGATSLCFVYPLDFARTRLADVKGAGAEERFGLGDLVYKSDGKGLYQGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVKGAGAEERFGLGDLVYKSDGKGLYQGFNVS 180

QY 181 VGGIIIRAAVFGIYDTAKMLDPKNTHTVISMIAQYTAAGLTSYFDDVRRMM 240
 FT 181 VGGIIIRAAVFGIYDTAKMLDPKNTHTVISMIAQYTAAGLTSYFDDVRRMM 240
 DB 181 VGGIIIRAAVFGIYDTAKMLDPKNTHTVISMIAQYTAAGLTSYFDDVRRMM 240

QY 241 QSGRKGDIMVTGTLDCWRKIARDEGKAFKGAWSNVLGMGAFVLYLDEIKKYYT 298
 FT 241 QSGRKGDIMVTGTLDCWRKIARDEGKAFKGAWSNVLGMGAFVLYLDEIKKYYT 298
 DB 241 QSGRKGDIMVTGTLDCWRKIARDEGKAFKGAWSNVLGMGAFVLYLDEIKKYYT 298

RESULT 2
 ADT2_RAT
 ID ADT2_RAT STANDARD; PRT; 298 AA.
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.",
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: D12771; BAA02238.1; -
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr. 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT SEQUENCE 298 AA; 32901 MW; 6A59204B987E9E35 CRC64;

Query Match 98.6%; Score 1525; DB 1; Length 298;
 Best local Similarity 98.3%; Pred. No. 1.1e-128;
 Matches 293; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTPAALSFADFLAGVAAAIKSTAVAPIERVKLLQVGHASKQTADKQYKGIIDCVR 60
 FT 1 MTPAALSFADFLAGVAAAIKSTAVAPIERVKLLQVGHASKQTADKQYKGIIDCVR 60
 DB 1 MTPAALSFADFLAGVAAAIKSTAVAPIERVKLLQVGHASKQTADKQYKGIIDCVR 60

QY 61 IPKEOVLSTFWRGNLANVIRYPTQALNFAFKYKQIFLGVDKRTQFWRYPAGNLASG 120
 FT 61 IPKEOVLSTFWRGNLANVIRYPTQALNFAFKYKQIFLGVDKRTQFWRYPAGNLASG 120
 DB 61 IPKEOVLSTFWRGNLANVIRYPTQALNFAFKYKQIFLGVDKRTQFWRYPAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRLADVKGAGAEERFGLGDLVYKSDGKGLYQGFNVS 180
 FT 121 GAAGATSLCFVYPLDFARTRLADVKGAGAEERFGLGDLVYKSDGKGLYQGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVKGAGAEERFGLGDLVYKSDGKGLYQGFNVS 180

QY 181 VGGIIIRAAVFGIYDTAKMLDPKNTHTVISMIAQYTAAGLTSYFDDVRRMM 240
 FT 181 VGGIIIRAAVFGIYDTAKMLDPKNTHTVISMIAQYTAAGLTSYFDDVRRMM 240
 DB 181 VGGIIIRAAVFGIYDTAKMLDPKNTHTVISMIAQYTAAGLTSYFDDVRRMM 240

QY 241 QSGRKGDIMVTGTLDCWRKIARDEGKAFKGAWSNVLGMGAFVLYLDEIKKYYT 298
 FT 241 QSGRKGDIMVTGTLDCWRKIARDEGKAFKGAWSNVLGMGAFVLYLDEIKKYYT 298
 DB 241 QSGRKGDIMVTGTLDCWRKIARDEGKAFKGAWSNVLGMGAFVLYLDEIKKYYT 298

RESULT 3
ADP2_MOUSE STANDARD: PRT: 298 AA.
ID ADP2_MOUSE PRT: 298 AA.
AC P51881; Q61311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RL homologs.";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Cochet P.; Laplace C.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP REVISIONS.
RA Laplace C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20432087; PubMed=10974536;
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RL translocase 1 and 2 genes.";
RN [6]
RL Gene 254:57-66(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U27316; AAC52838.1; -;
DR EMBL: U10404; AAA19009.1; -;
DR EMBL: X70847; CAA50196.1; -;
DR EMBL: AF240003; AAF64471.1; -;
DR MGD: MGI:1353496; SLC25A5.
DR InterPro: IPR002067; MLC_carrier.
DR InterPro: IPR001993; MitoCh_carrier.
DR Pfam: PF00153; mito_carr.3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER.3.
KM Mitochondrion, inner membrane; Repeat: Transmembrane; Transport;
KW Multigene family.
FT 12 29 1 (POTENTIAL).

FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32931 MM; 0798E04B987EFE20 CRC64;
Query Match 98.2%; Score 1519; DB 1; Length 298;
Best Local Similarity 98.0%; Pred. No.3-8e-128;
Matches 292; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 MTDALSPKDFLAGVAAISKTAVERKLLQVHASKQTADKQYGIIDCVR 60
DB 1 MTDAAVSFAKDFLAGVAAISKTAVERKLLQVHASKQTADKQYGIIDCVR 60
QY 61 IPKEDEVLSFWGNNLVNRYRFPQTALNFAFKDKYKQIFLGVDKRTQWRFAGNLASG 120
DB 61 IPKEDEVLSFWGNNLVNRYRFPQTALNFAFKDKYKQIFLGVDKRTQWRFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADYKAGAEERFGDCLVKIKYSDGIRKGLYGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTLADYKAGAEERFGDCLVKIKYSDGIRKGLYGFNVS 180
QY 181 VGGIIIRRAAYGIYDTAKGLPDPKNTIIVISMIATQVTAVAGLTSTYPTVRRRM 240
DB 181 VGGIIIRRAAYGIYDTAKGLPDPKNTIIFISMAIQSVTAAGLTSTYPTVRRRM 240
QY 241 QSGRGTDTIMYGTLDCKWKIARDDEGKAFEGGANSNVIRGSGAFVLVLYEIRK 298
DB 241 QSGRGTDTIMYGTLDCKWKIARDDEGKAFEGGANSNVIRGSGAFVLVLYEIRK 298
RESULT 4
ADP3_BOVIN STANDARD: PRT: 298 AA.
ID ADP3_BOVIN PRT: 298 AA.
AC P32007;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
DE nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RL differences in various tissues.";
RN [2]
RL Biochemistry 28:866-873(1989).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL: M24103; AAA30769.1; -.
 DR PIR: B43646; B43646.
 DR InterPro: IPR002067; MLC_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 2 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;
 Query Match 94.2%; Score 1458; DB 1; Length 298;
 Best Local Similarity 92.9%; Pred. No. 1e-122;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MTDALSFADFLAGVAAAIKTAAPVPIEVKLLQVHASKOITADKQYGIIDCVR 60
 DB 1 MTEQAIISFADFLAGVAAAIKTAAPVPIEVKLLQVHASKOITADKQYGIIDCVR 60
 QY 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
 DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
 QY 121 GAAGATSLCEFYPLDFAFRTIADLVGKAGAREFERGLGDCLVKTKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCEFYPLDFAFRTIADLVGKAGAREFERGLGDCLVKTKSDGKGLYOGFNVS 180
 QY 181 VQGIITIRAAAFGLYDPAKGMPLPKNTHTYISMMIAQTVAVALGSLSPYDTRRRMM 240
 DB 181 VQGIITIRAAAFGLYDPAKGMPLPKNTHTYISMMIAQTVAVALGSLSPYDTRRRMM 240
 QY 241 QSGRRKGDIMYTGTLDCWRKTADEGSKAFPKGAMSNVLRMGAGFVLVLDKIK 296
 DB 241 QSGRRKGDIMYTGTLDCWRKTADEGSKAFPKGAMSNVLRMGAGFVLVLDKIK 296
 RESULT 5
 ADT3_HUMAN STANDARD; PRT; 298 AA.
 ID ADT3_HUMAN STANDARD; PRT; 298 AA.
 AC P12236; Q96C49.
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
 DE (Adenine nucleotide translocator 3) (ANT 3).
 GN SLC25A6 OR ANT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN NCBI
 RP MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 ADP/ATP translocase";
 J. Mol. Biol. 206:261-280(1989).
 RP SEQUENCE FROM N.A.
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
 RA Margolin J.F.;
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RC TISSUE=Brain, Cervix, Eye, and Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Altairi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 level in adult human liver";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: J03592; AAA36750.1; -.
 DR EMBL: AY007135; AAG01998.1; -.
 DR EMBL: BC007295; AAH07295.1; -.
 DR EMBL: BC007850; AAH07850.1; -.
 DR EMBL: BC008737; AAH08737.1; -.
 DR EMBL: BC008935; AAH08935.1; -.
 DR EMBL: BC014775; AAH14775.1; -.
 DR PIR: S03894; S03894.
 DR PIR: B28116; B28116.
 DR Genew; HGNC:10992; SLC25A6.
 DR MIM; 300151; -.
 DR MIM; 403000; -.
 DR InterPro: IPR002067; MLC_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 105 108 3.
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
 FT SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;
 Query Match 94.0%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 2.3e-122;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTDALSFADFLAGVAAAIKTAAPVPIEVKLLQVHASKOITADKQYGIIDCVR 60
 DB 1 MTEQAIISFADFLAGVAAAIKTAAPVPIEVKLLQVHASKOITADKQYGIIDCVR 60
 QY 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
 DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
 QY 121 GAAGATSLCEFYPLDFAFRTIADLVGKAGAREFERGLGDCLVKTKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCEFYPLDFAFRTIADLVGKAGAREFERGLGDCLVKTKSDGKGLYOGFNVS 180

```

Db 121 GAAGATSLCFVYPLDPARTRLAADVKGSGTEREFGDGLVKITKSDCIRGLYOGFSVS 180
Qy 181 VGGIIIRAAVFGYDFAKGMLEDPKNTNHIIVSMIAQVTAVAGLTSYPTDTRRRMM 240
Db 181 VGGIIIRAAVFGYDFAKGMLEDPKNTNHIIVSMIAQVTAVAGVSYPTDTRRRMM 240
Qy 241 OSGRKGTDMYGTGLDCMRKRIARDEGKAFKFGAMSNVLRMGAGFVLYLYDEIKK 296
Db 241 OSGRKADIMYGTGLDCMRKRIARDEGKAFKFGAMSNVLRMGAGFVLYLYDELK 296

RESULT 6
ADTL_MOUSE
ID ADTL_MOUSE STANDARD: PRT: 298 AA.
AC P48962; Q62164;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).
GN SLC25A4 OR ANT1 OR ANCL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudoautosomal genes and their mouse homologs."
RL Mann. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Muscle;
RA Laplace C., Costet P.;
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes."
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U27315; AAC52837.1; -.
CC EMBL: X74510; CA552616.1; -.
CC EMBL: AF240002; AAF64470.1; -.
CC EMBL: BC003791; AAH03791.1; -.
CC EMBL: BC026925; AAH26925.1; -.
CC MGD: MGI:1353495; SLC25A4.
CC InterPro: IPR002067; MLC_carrier.
CC InterPro: IPR001993; Mitoch_carrier.

```

```

DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multi-gene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 136 136 F -> L (IN REF. 1).
SQ SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match
Best Local Similarity 91.6%; Score 1417; DB 1; Length 298;
Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MTDALSPAKDEFLAGVAAAIKSTAVAPIERYKLLQVQHASKQTADKQYGIIDCVVR 60
Db 1 MGDQALSLFKDLFLAGIAAASKTAVAPIERYKLLQVQHASKQIAEKQYGIIDCVVR 60
Qy 61 IREDEVLSFWRGNLANVIRPEPTQALNFAFDKTKQITGLGVYDKRTQWRIFAGNLASG 120
Db 61 IREDEVLSFWRGNLANVIRPEPTQALNFAFDKTKQITGLGVYDKRTQWRIFAGNLASG 120
Qy 121 GAAGATSLCFVYPLDPARTRLAADVKGASERFGLGCLVITYKYSDDGIRKLGQFNVNS 180
Db 121 GAAGATSLCFVYPLDPARTRLAADVKGSSQRFNGLGCLTKIRFSDGLKLGQFVS 180
Qy 181 VGGIIIRAAVFGYDFAKGMLEDPKNTNHIIVSMIAQVTAVAGLTSYPTDTRRRMM 240
Db 181 VGGIIIRAAVFGYDFAKGMLEDPKNTNHIIVSMIAQVTAVAGVSYPTDTRRRMM 240
Qy 241 OSGRKGTDMYGTGLDCMRKRIARDEGKAFKFGAMSNVLRMGAGFVLYLYDEIKK 297
Db 241 OSGRKADIMYGTGLDCMRKRIARDEGKAFKFGAMSNVLRMGAGFVLYLYDEIKK 297

RESULT 7
ADTL_RAT
ID ADTL_RAT STANDARD: PRT: 298 AA.
AC Q05962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shiohara Y., Kamada M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator."
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER EXTENT, IN BRAIN AND KIDNEY.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X61667; CAA43842.1; -
DR EMBL: D12770; BAA02237.1; -
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FE78C6BC320 CRC64;

Query Match 91.6%; Score 1417; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 4.7e-119;
Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

OY 1 MTDALSFARDFLAGVAAATSKTAVAPIERVKLLLOVONHASKOTAPADKOVGIIDCVVR 60
DB 1 MGDAALSFLEDFLAGVAAATSKTAVAPIERVKLLLOVONHASKOISAEKQYKGIIDCVVR 60
OY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGVDKRTQFMRYFAGNLSAG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGVDVRRHGFMYFAGNLSAG 120
OY 121 GAAGATSLCFYPLDPARTRLADYVGKAGARERGLDCLVKYKSDGKIGLYOGFNVS 180
DB 121 GAAGATSLCFYPLDPARTRLADYVGKSGQREFNGLDCLTKLFKSDGLGLQGFVS 180
OY 181 VQGIITIRAAVFGIYDPAKGMLPKKNTHIYSMIAQTVAVAGLTSYPTDVRRRMM 240
DB 181 VQGIITIRAAVFGIYDPAKGMLPKKNTHIYSMIAQTVAVAGLTSYPTDVRRRMM 240
OY 241 QSGRKGFDIMYTGTLDCWRKIARDGSKAFPKGAMSNVLRMGAFVLVLYDEIKKY 297
DB 241 QSGRKGADIMYTGTVDCWRKIARDGSKAFPKGAMSNVLRMGAFVLVLYDEIKKY 297

RESULT 8
ADTL_BOVIN STANDARD; PRT; 297 AA.
ID ADTL_BOVIN
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86229093; PubMed=2540808;
* Powell S.J., Mead S.M., Runswick M.J., Walker J.E.;

```

```

RT "two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
RN [2]
RP SEQUENCE
RX MEDLINE=82186267; PubMed=7076130;
RA Aquila H., Mista D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13783; AAA30363.1; -
DR EMBL: M24102; AAA30768.1; -
DR PIR: A03181; XMO.
DR PIR: A24822; A24822.
DR PIR: A43646; A43646.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT INT_MET 0 0
FT MOD_RES 1 1 BLOCKED.
FT TRANSMEM 51 51 1 (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AE848 CRC64;

Query Match 91.4%; Score 1414; DB 1; Length 297;
Best Local Similarity 89.9%; Pred. No. 8.6e-119;
Matches 266; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

OY 2 TDAALSFARDFLAGVAAATSKTAVAPIERVKLLLOVONHASKOTAPADKOVGIIDCVRI 61
DB 1 SDQALSFLEDFLAGVAAATSKTAVAPIERVKLLLOVONHASKOISAEKQYKGIIDCVRI 60
OY 62 IPKEQEVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGVDKRTQFMRYFAGNLSAG 121
DB 62 IPKEQGLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGVDVRRHGFMYFAGNLSAG 120
OY 122 AAGATSLCFYPLDPARTRLADYVGKAGARERGLDCLVKYKSDGKIGLYOGFNVS 181
DB 122 AAGATSLCFYPLDPARTRLADYVGKAGARERGLDCLVKYKSDGKIGLYOGFNVS 181

```

DB 121 AAGATSLCFVYPLDPAFRLADVGKGAQREFGLGNCITKIFKSDGLRGLYQGFNVSV 180
 QY 182 QGIIITTYRAAYFGIYDTAKGMLDPKPNTHIVISMIAQVTAVAGLTSYFPDTRRRMMQ 241
 DB 181 QGIIITTYRAAYFGIYDTAKGMLDPKPNTHIVISMIAQVTAVAGLTSYFPDTRRRMMQ 240
 QY 242 SRRKGTDIWYTGTLGCMRKRIARDEGGKAFKFGKAMSNTVLGGAFLVLYDEIKKK 297
 DB 241 SRRKADIMYTGTVCCWKRRIANDEGPKAFKFGKAMSNTVLGGAFLVLYDEIKKF 296

RESULT 9
 ADP1_HUMAN
 ID ADP1_HUMAN STANDARD: PRT: 298 AA.
 AC P12235;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89340499; PubMed=2547778;
 RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
 RT "A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed.";
 RL J. Biol. Chem. 264:13936-14004(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041149; PubMed=2823266;
 RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
 RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RT Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-37 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 RN [6]
 RP VARIANTS PRO-114 AND MET-289
 RX MEDLINE=20385067; PubMed=10925541;
 RA Kauonen J., Juselius J.K., Tiranli V., Kytala A., Zeviani M., Cont G.P., Kepanen J., Peltonen L., Suomalainen A.;
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
 RL Science 289:782-785(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J02966; AAA61223.1; -;
 DR EMBL: J03593; AAA36751.1; -;
 DR EMBL: J04982; AAA51736.1; -;
 DR EMBL: BC008664; AAH08664.1; -;
 DR PIR: A28116; A28116.
 DR PIR: A39891; A39891.
 DR PIR: S03893; S03893.
 DR PIR: A44778; A44778.
 DR GeneW: HGNC:10990; SLC25A4.
 DR MIM: 103220; -;
 DR MIM: 157640; -;
 DR InterPro: IPR002067; MLC carrier.
 DR InterPro: IPR001993; Mitoch carrier.
 DR Pfam: PF00153; mito_carr. 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR KMW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family; Disease mutation.
 FT TRANSMEM 12 29
 FT TRANSMEM 73 91 1 (POTENTIAL).
 FT TRANSMEM 117 134 2 (POTENTIAL).
 FT TRANSMEM 176 195 3 (POTENTIAL).
 FT TRANSMEM 214 231 4 (POTENTIAL).
 FT TRANSMEM 273 291 5 (POTENTIAL).
 FT REPEAT 1 110 6 (POTENTIAL).
 FT REPEAT 111 208 1.
 FT REPEAT 209 298 2.
 FT REPEAT 114 114 3.
 FT VARIANT 289 289
 FT VARIANT
 FT VARIANT
 FT CONFLICT 16 16 A -> P (IN PEO).
 FT CONFLICT 147 149 G -> A (IN PEO).
 FT CONFLICT 227 227 V -> M (IN PEO).
 FT CONFLICT 227 227 KCA -> RR (IN REF. 3).
 FT CONFLICT 227 227 V -> L (IN REF. 3).
 SQ SEQUENCE 298 AA; 33064 MW; 59F0DFEACE4ETCFBB CRC64;

Query Match 91.3%; Score 1413; DB 1; Length 298;
 Best Local Similarity 89.2%; Pred No. 1; 1e-118;
 Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDELAGVAAIAISKTAVALPIERYKLLQVOHASKQTADKQYKGIIDCVVR 60
 DB 1 MCDHAWSLFKDLFLAGVAAVASKTAVAPIERYKLLQVOHASKQISAEKQYKGIIDCVVR 60
 QY 61 IRKEDEVLSEFWRGNLNANVIRFPTQALNFAFDKXKQITFLGVDKRTQWRPFAGLNLASG 120
 DB 61 IRKEDEVLSEFWRGNLNANVIRFPTQALNFAFDKXKQITFLGVDKRTQWRPFAGLNLASG 120
 QY 121 GAAGATSLCFVYPLDPAFRLADVGKGAQREFGLGNCITKIFKSDGLRGLYQGFNVSV 180
 DB 121 GAAGATSLCFVYPLDPAFRLADVGKGAQREFGLGNCITKIFKSDGLRGLYQGFNVSV 180
 QY 181 VOGIIITTYRAAYFGIYDTAKGMLDPKPNTHIVISMIAQVTAVAGLTSYFPDTRRRMMQ 240
 DB 181 VOGIIITTYRAAYFGIYDTAKGMLDPKPNTHIVISMIAQVTAVAGLTSYFPDTRRRMMQ 240

RESULT 11

```

ADT_ANOGA          STANDARD:          PRT:          301 AA.
ID ADT_ANOGA
AC Q27238:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Culicoides; Anophelinae.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G3:
RX MEDLINE=94348635; PubMed=8069414;
RA Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;
RT "A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles
gambiae."
RL Insect Mol. Biol. 3:35-40(1994).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sdb.ch/announce/
or send an email to license@sdb-sdb.ch).
-----
CC EMBL: L11618; AAB04104.1; -.
CC EMBL: L11617; AAB04105.1; -.
CC InterPro: IPR002067; Mlt_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_carr; 3.
CC PRINTS: PR00926; MITOCARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 3.
CC Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport.
CC TRANSMEM 14 31 1 (POTENTIAL).
CC TRANSMEM 75 93 2 (POTENTIAL).
CC TRANSMEM 119 136 3 (POTENTIAL).
CC TRANSMEM 178 197 4 (POTENTIAL).
CC TRANSMEM 216 233 5 (POTENTIAL).
CC TRANSMEM 275 293 6 (POTENTIAL).
CC TRANSMEM 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;
SQ SEQUENCE
Query Match 76.9%; Score 1190; DB 1; Length 301;
Best Local Similarity 78.8%; Pred. No. 8e-99;
Matches 227; Conservative 18; Mismatches 43; Indels 0; Gaps 0;

```

```

DB 190 RAAYFGCEFTAGKMLPDPKNTHTLVISMIAQVTTAVAGLTSYPTDVRRRMMMQSRKGT 249
OY 248 DIMYGTGLDCCWKKIARDEGGKAEFGGAWSNVLKMGCAFVLYDEIK 295
DB 250 EVMYKNTLDCWVKIGKQEGSGAFAFGKAFSNVLRTGCGALVLYFEYDEVK 297

```

RESULT 12

```

ADT_CHLKE          STANDARD:          PRT:          339 AA.
ID ADT_CHLKE
AC P31692:
DT 01-JUL-1993 (Rel. 26, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
OS Chlorella kessleri.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Chlorella.
OX NCBI_TaxID=3074;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92084708; PubMed=1748677;
RA Hilgarch C., Sauer N., Tanner W.;
RT "Glucose increases the expression of the ATP/ADP translocator and the
glyceralddehyde-3-phosphate dehydrogenase genes in Chlorella."
RL J. Biol. Chem. 266:24044-24047(1991).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sdb.ch/announce/
or send an email to license@sdb-sdb.ch).
-----
CC EMBL: M76669; AAA33027.1; -.
CC PIR: A41677; A41677.
CC InterPro: IPR002067; Mlt_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_carr; 3.
CC PRINTS: PR00926; MITOCARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 3.
CC Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport.
CC TRANSMEM 45 62 1 (POTENTIAL).
CC TRANSMEM 108 126 2 (POTENTIAL).
CC TRANSMEM 151 168 3 (POTENTIAL).
CC TRANSMEM 209 228 4 (POTENTIAL).
CC TRANSMEM 248 265 5 (POTENTIAL).
CC TRANSMEM 304 322 6 (POTENTIAL).
CC TRANSMEM 339 AA; 36686 MW; 54779734A3B3942 CRC64;
SQ SEQUENCE
Query Match 62.6%; Score 968; DB 1; Length 339;
Best Local Similarity 65.8%; Pred. No. 5.6e-79;
Matches 194; Conservative 29; Mismatches 64; Indels 8; Gaps 5;

```

```

Db 158 GAGSLIVPLDFAKRLADVG-SGKSRFTGVLVDLSKVKKRGPMALYOGFVSGV 216
QY 184 IIVRAAYFGIYDTAKML-PDPKNTHTIVISMIAQVTAVAGLTSYPTDVRMRM 242
Db 217 IIVRGAYFGIYDTAKMLPDEKNTANFPAKMAVAQAVTAGAGLSTPFDVRRRLM 276
QY 243 GRKGTDMITGTLDCKRKIRADEGGAFFKAGMSNVLRGMAFVLVLYDEIKRY 297
Db 277 ---GGERQYNGTIDCMRKVAQOEGKMAFFKAGMSNVLRGAGAVLVLYDEIKRF 328

RESULT 13
ADT1_GOSHI STANDARD; PRT; 386 AA.
ID ADT1_GOSHI STANDARD; PRT; 386 AA.
AC 02342;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP, ATP carrier protein 1, mitochondrial precursor (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN ANT1.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Texas Marker 1; TISSUE=Fiber;
RA Shin H., Brown R.M. Jr.;
RT "Two cDNA sequences for the adenine nucleotide translocator, CAN1 and CAN2, from cotton fibers (Gossypium hirsutum).";
RL (In) Plant Gene Register PGR97-130.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF006489; AAB72047.1; -
DR InterPro: IPR002067; MitCarrier.
DR InterPro: IPR001993; MitochCarrier.
DR Pfam: PF00153; mito-cartr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 2.
KM Mitochondrion: Inner membrane: Repeat; Transmembrane; Transport; Transist peptide; Multigene family.
FT TRANSIT 1 76
FT CHAIN 1 386 MITOCHONDRION (BY SIMILARITY).
FT TRANSMEM 77 386 ADP, ATP CARRIER PROTEIN 1.
FT TRANSMEM 90 107 1 (POTENTIAL).
FT TRANSMEM 152 170 2 (POTENTIAL).
FT TRANSMEM 195 212 3 (POTENTIAL).
FT TRANSMEM 256 275 4 (POTENTIAL).
FT TRANSMEM 295 312 5 (POTENTIAL).
FT TRANSMEM 351 369 6 (POTENTIAL).
SQ SEQUENCE 386 AA; 42093 MW; A05F76C73FFED66 CRC64;

Query Match 49.8%; Score 771; DB 1; Length 386;
Best Local Similarity 55.4%; Pred. No. 2,4e-61;
Matches 165; Conservative 33; Mismatches 79; Indels 22; Gaps 7;
QY 7 SFANDFLAGVAIAIKTAVAPIERVKLLQV-HASKQITADKQYGIIDCVRIPEEQ 65
Db 85 SFALDILMGVSAVSKTAAPRIERVKLLQNDQEMIKSGRLSPYKIGGCFRRTIKDE 144
QY 66 EVLSFMGNLANVIRPEPTQALNFAFKDKYKQITLGGVDRKRTQFWRIFAGNLASGAGA 125

```

```

Db 145 GFGSLMKGNTANVIRPEPTQALNFAFDYKRLFNPKKD-RDGWKWFAQNLASGAGA 203
QY 126 TSICEFVYPLDPAFRLAD--VKGASERFERGGIDCLVTKYSKGILKYOGNNVSG 183
Db 204 SSLFVTSLDPAFRLANDAKAKKGGROPNGLVYRRTKLSGDLGAGLKGFNISCVG 263
QY 184 IIVRAAYFGIYDTAK-----GMLPDPKNTHTIVISMIAQVTAVAGLTSYPTDVRMRM 238
Db 264 IIVRGAYFGIYDTAKLVLLTSGMQDSEFPASVILGWL-----TNGALASYPIDTVRRM 319
QY 239 MMGSRKGTDMITGTLDCKRKIRADEGGAFFKAGMSNVLRGMAFVLVLYDET----- 294
Db 320 MMTSGKA---VKRKSLSDAFSQILKNEGKSLFKAGSNILRLAAGAGVLGYDKQLIIV 376
QY 295 --KKY 297
Db 377 FGKKY 381

RESULT 14
ADT1_SCHPO STANDARD; PRT; 322 AA.
ID ADT1_SCHPO STANDARD; PRT; 322 AA.
AC 009186;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP, ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
GN ANCI OR SPBC530.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=96257204; PubMed=8675018;
RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae.";
RL Gene 171:113-117(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymprez B., Welteens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Sipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";

```

RL Nature 415:871-880(2002).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: 249974; CAA90275.1; -
CC DR EMBL: AL023634; CAA19176.1; -
CC DR InterPro: IPR002067; Mit_carrier.
CC DR InterPro: IPR001993; Mitoch_carrier.
CC DR Pfam: PF00153; mito_carrier; 3.
CC DR PRINTS: PR00926; MITOCARRIER.
CC DR PROSITE: PS00215; MITOCH_CARRIER; 2.
CC KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
CC FT TRANSMEM 28 48 1 (POTENTIAL).
CC FT TRANSMEM 93 111 2 (POTENTIAL).
CC FT TRANSMEM 131 151 3 (POTENTIAL).
CC FT TRANSMEM 197 217 4 (POTENTIAL).
CC FT TRANSMEM 222 242 5 (POTENTIAL).
CC FT TRANSMEM 289 309 6 (POTENTIAL).
CC SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A0F41AFC CRC64;

Query Match 49.8%; Score 770; DB 1; Length 322;
Best Local Similarity 53.6%; Pred. No. 2.3e-61;
Matches 158; Conservative 51; Mismatches 74; Indels 12; Gaps 6;

QY 7 SFAKPLAGVAAAIKSTVAPIERVKLLQVHASKQTADK---QYKGIIDCVVRIRK 63
DB 26 TFFEFMMGSAVAASKTAAPIERVKLLIQND---DEMIRAGRLSHRYKIGCECFRTAA 83
QY 64 EOEVSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRTPQWRFAGNLASGAA 123
DB 84 EECGVLSMRGNANVLRIFPTQALNFAFKDKKMF--GKKERDGYAKKFAGNLASGAA 142
QY 124 GATSLCEFYVPLDFARTLAADY--GKAGAREERGLGDCLVKIKSDGIGLYOGFNVSQ 181
DB 143 GASLLEFYVSLDYARTRLANDAKSAKKGGEQFNGLVYRRTYRSDGLRGYRGFSPV 202
QY 182 QGIIIRAYAFGIYDTAKG--MLPDKNTHIVISMIAQVTAVAGLTSYPTQVRRRMM 240
DB 203 VGIIVYRGILYFGMYDTLKVVLVGLPGLGNFLASFLLGMVNTGSGVASYPPLDIRRRMM 262
QY 241 QSGRGTDMYGTGLDCMRKIARDEGKAFFKAGMSVNLRGMGAFVLYLDEIK 295
DB 263 TSGEA---VKYSSFECCGRIILAKBEGARSEFFKAGANILRGVAGAVLSIYQVQ 314

RESULT 15
ADT_CHLRE STANDARD: PRT: 308 AA.
AC P27080:
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
DE translocator) (ANT).
GN ABT.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-FUD4-R2;
RX MEDLINE-93204887; PubMed=8455552;
RA Shaire J.A., Day A.;
RT "Structure, evolution and expression of the mitochondrial ADP/ATP
RT translocator gene from Chlamydomonas reinhardtii";
RL Mol. Gen. Genet. 237:114-144(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: X65194; CAA46311.1; -
CC DR PIR: S30259; S30259.
CC DR InterPro: IPR002067; Mit_carrier.
CC DR InterPro: IPR001993; Mitoch_carrier.
CC DR Pfam: PF00153; mito_carrier; 3.
CC DR PRINTS: PR00926; MITOCARRIER.
CC DR PROSITE: PS00215; MITOCH_CARRIER; 2.
CC KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
CC FT TRANSMEM 12 29 1 (POTENTIAL).
CC FT TRANSMEM 74 92 2 (POTENTIAL).
CC FT TRANSMEM 116 133 3 (POTENTIAL).
CC FT TRANSMEM 178 197 4 (POTENTIAL).
CC FT TRANSMEM 217 234 5 (POTENTIAL).
CC FT TRANSMEM 273 291 6 (POTENTIAL).
CC SQ SEQUENCE 308 AA; 33528 MW; D477CE0E7B753F CRC64;

Query Match 49.5%; Score 765; DB 1; Length 308;
Best Local Similarity 52.6%; Pred. No. 6.2e-61;
Matches 159; Conservative 49; Mismatches 78; Indels 16; Gaps 6;

QY 7 SFAKPLAGVAAAIKSTVAPIERVKLLQVHASKQTADKQYKGIIDCVVRIRK 65
DB 7 NFWYDFLAGLSAAVSKTAAPIERVKLLIQNDEMIRAGRLSPYKIGCECFRTVREE 66
QY 66 EYLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRTPQWRFAGNLASGAA 125
DB 67 GCGSLMRGNANVLRIFPTQALNFAFKDKKMF--GPKKREYKMFAGNMAASGAGA 124
QY 126 TSLCEFYVPLDFARTLAAD--VGKAGAREERGLGDCLVKIKSDGIGLYOGFNVSQ 182
DB 125 VSLSEFYVSLDYARTRLANDAKSAKKGGEQFNGLVYRRTYRSDGLRGYRGFISCV 184
QY 183 GIIRAYAFGIYDTAKG--MLPDKNTHIVISMIAQVTAVAGLTSYPTQVRRRMM 241
DB 185 GIIVYRGILYFGMYDTLKVVLVGLPGLGNFLASFLLGMVNTGSGVASYPPLDIRRRMM 244
QY 242 SGRKGTDMYGTGLDCMRKIARDEGKAFFKAGMSVNLRGMGAFVLYLDEI-----K 295
DB 245 S---GSAVYVNSSFHCFQELVYKNEGKMSLFKAGANILRGVAGAVLSDQVLLSK 301
QY 296 KY 297
DB 302 KY 303

Search completed: November 12, 2002, 16:46:27
Job time : 8.67525 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:45 ; Search time 25.3617 Seconds
(without alignments)
2421.054 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547
Sequence: 1 MTDALSPFAKDFLAGGVAAA.....LKGMGAFVLYLDEIKKTT 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

SPREMBL.21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1515	97.9	298	6	08SQH5
2	1446	93.5	298	13	09PRH1
3	1443	93.3	298	13	09PRH2
4	1439	93.0	298	13	09YIC4
5	1425	92.1	298	13	0919M9
6	1423	92.0	298	6	046373
7	1417	91.6	298	11	062164
8	1295	83.7	317	13	091336
9	1278	82.6	299	5	095VX4
10	1253.5	81.0	299	5	095S30
11	1248.5	80.7	300	5	09NH55
12	1190.5	77.0	288	5	044093
13	1185.5	76.6	288	5	044094
14	1145.5	74.0	304	5	025129
15	1125.5	72.8	307	5	062526
16	1102	71.2	315	4	09HOC2

17	1032	66.7	300	5	045865	045865 caenorhabd1
18	1029	66.5	313	5	P91410	P91410 caenorhabd1
19	1029	66.5	313	5	021103	021103 caenorhabd1
20	986	63.7	300	5	001813	001813 caenorhabd1
21	985	63.7	309	5	097470	097470 dictyostell
22	983	63.5	300	5	017407	017407 caenorhabd1
23	950.5	61.4	318	5	09B336	09B336 toxoplasma
24	949.5	61.4	307	8	09XM22	09XM22 ascaris suu
25	939	60.7	301	5	025692	025692 plasmodium
26	938	60.6	301	5	026006	026006 plasmodium
27	819	52.9	170	6	09XS69	09XS69 sus scrofa
28	778	50.3	305	3	09P8M1	09P8M1 yarrowia 11
29	759	49.1	326	5	P91270	P91270 caenorhabd1
30	755	48.8	303	3	074260	074260 candida par
31	753	48.7	317	5	09N647	09N647 leishmania
32	752	48.6	307	5	076286	076286 trypanosoma
33	750	48.5	386	10	P93767	P93767 lycopersico
34	749.5	48.4	306	5	018683	018683 caenorhabd1
35	747	48.3	388	10	049875	049875 lupinus alb
36	746	48.2	306	3	P78754	P78754 schizosacch
37	746	48.2	379	10	049447	049447 arabidopsis
38	745	48.2	307	5	026697	026697 trypanosoma
39	740	47.8	331	10	041628	041628 triticum tu
40	721.5	46.6	305	3	09P876	09P876 pichia jadt
41	718.5	46.4	305	3	09P875	09P875 pichia jadt
42	717.5	46.4	308	3	08TFA7	08TFA7 neocallimas
43	690.5	44.6	330	10	09FPM8	09FPM8 arabidopsis
44	665.5	43.0	298	5	021809	021809 caenorhabd1
45	656.5	42.4	262	10	09AVT6	09AVT6 picea abies

ALIGNMENTS

RESULT 1
08SQH5 PRELIMINARY; PRT; 298 AA.
ID 08SQH5;
AC 08SQH5;
DT 01-JUN-2002 (TREMUREL. 21, Created)
DT 01-JUN-2002 (TREMUREL. 21, Last sequence update)
DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)
DE Adenine nucleotide translocator 2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT Identification of possible amino acids that determine functional
RT differences in its isoforms";
RL Mitochondrion 1:371-379(2002).
DR EMBL: AB065433; BAB84673.1; -;
SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match 97.9%; Score 1515; DB 6; Length 298;
Best Local Similarity 97.7%; Pred. No. 4.8e-126;
Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 MTDALSPFAKDFLAGGVAAAIKRAVAPRIERVKLLLOVHASKRITADKQYKGIIDCVR 60
Db 1 MTDALSPFAKDFLAGGVAAAIKRAVAPRIERVKLLLOVHASKRITADKQYKGIIDCVR 60
QY 1PKKOEVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGGVGRPTQFMRYFAGNLASG 120
Db 1PKKOEVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGGVGRPTQFMRYFAGNLASG 120
QY 121 GAAGATSLCFYYPPLDFKARTLADYVKGAGAEERERGLGDCLVKTKSDGKGLGYGNVS 180
Db 121 GAAGATSLCFYYPPLDFKARTLADYVKGAGAEERERGLGDCLVKTKSDGKGLGYGNVS 180

CY 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWMIAGTVAAGLTSYPTDTRRRMM 240
 DB 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWMIAGTVAAGLTSYPTDTRRRMM 240
 CY 241 QSGRGKTDIMYGTLDCKMKIARDGSGKAFKFGAMSNTLRGAGAVLVLYDEIKKY 298
 DB 241 QSGRGKTDIMYGTLDCKMKIARDGSGKAFKFGAMSNTLRGAGAVLVLYDEIKKY 298

RESULT 2

Q9PRH1 PRELIMINARY; PRT; 298 AA.
 AC Q9PRH1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99083429; PubMed-9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorph sex chromosomes
 of 2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008463; BAA36510.1; -;
 DR EMBL; AB008456; BAA36508.1; -;
 DR EMBL; AB008461; BAA36511.1; -;
 DR EMBL; AB008462; BAA36512.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR002030; Mlt_uncoupling.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 93.5%; Score 1446; DB 13; Length 298;
 Best Local Similarity 91.9%; Pred. No. 6, 2e-120;
 Matches 273; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTDALSFAPKDFLAGVAAIAISKTAVAPTERYKLLQVGHASKQITADKQYGIIDCVR 60
 DB 1 MTDALSFAPKDFLAGVAAIAISKTAVAPTERYKLLQVGHASKQITADKQYGIIDCVR 60
 QY 61 IREDEVSFWMGNLANVIRYPTQALNFAFKDKYKIFLDNVDRKTFWRFFAGNLASG 120
 DB 61 IREDEVSFWMGNLANVIRYPTQALNFAFKDKYKIFLDNVDRKTFWRFFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPAFRLAADVGKAGAREFRGLGDLVKIYSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDPAFRLAADVGKAGAREFRGLGDLVKIYSDGKGLYOGFNVS 180
 QY 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWMIAGTVAAGLTSYPTDTRRRMM 240
 DB 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWMIAGTVAAGLTSYPTDTRRRMM 240
 QY 241 QSGRGKTDIMYGTLDCKMKIARDGSGKAFKFGAMSNTLRGAGAVLVLYDEIKKY 297
 DB 241 QSGRGKTDIMYGTLDCKMKIARDGSGKAFKFGAMSNTLRGAGAVLVLYDEIKKY 297

RESULT 3
 Q9PRH2

ID Q9PRH2 PRELIMINARY; PRT; 298 AA.
 AC Q9PRH2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99083429; PubMed-9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorph sex chromosomes
 of 2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008460; BAA36510.1; -;
 DR EMBL; AB008458; BAA36508.1; -;
 DR EMBL; AB008459; BAA36509.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR002030; Mlt_uncoupling.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 93.3%; Score 1443; DB 13; Length 298;
 Best Local Similarity 91.6%; Pred. No. 1, 1e-119;
 Matches 272; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTDALSFAPKDFLAGVAAIAISKTAVAPTERYKLLQVGHASKQITADKQYGIIDCVR 60
 DB 1 MTDALSFAPKDFLAGVAAIAISKTAVAPTERYKLLQVGHASKQITADKQYGIIDCVR 60
 QY 61 IREDEVSFWMGNLANVIRYPTQALNFAFKDKYKIFLDNVDRKTFWRFFAGNLASG 120
 DB 61 IREDEVSFWMGNLANVIRYPTQALNFAFKDKYKIFLDNVDRKTFWRFFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPAFRLAADVGKAGAREFRGLGDLVKIYSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDPAFRLAADVGKAGAREFRGLGDLVKIYSDGKGLYOGFNVS 180
 QY 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWMIAGTVAAGLTSYPTDTRRRMM 240
 DB 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWMIAGTVAAGLTSYPTDTRRRMM 240
 QY 241 QSGRGKTDIMYGTLDCKMKIARDGSGKAFKFGAMSNTLRGAGAVLVLYDEIKKY 297
 DB 241 QSGRGKTDIMYGTLDCKMKIARDGSGKAFKFGAMSNTLRGAGAVLVLYDEIKKY 297

RESULT 4
 Q9YIC4 PRELIMINARY; PRT; 298 AA.
 ID Q9YIC4;
 AC Q9YIC4;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE-99083429; PubMed-9866197;
 RA Mura I., Ohnani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 of 2, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008457; BAA36507.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mtc_carrier.
 DR InterPro: IPR002030; Mtc_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 33068 MW: 15B270ED37099A00 CRC64;

Query Match 93.0%; Score 1439; DB 13; Length 298;
 Best Local Similarity 91.2%; Pred. No. 2,6e-119;
 Matches 271; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

OY 1 MTDALSFADKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYKGIIDCVVR 60
 DB 1 MTDALISFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYKGIIDCVVR 60
 OY 61 IPKEDEVLSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLGVDKRTQFWRPAGNLASG 120
 DB 61 IPKEGDFVSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLGVDKRTQFWRPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFAPTRLAADYKAGAREFRGLGDCLYKIKSDGKLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFAPTRLAADYKAGAREFRGLGDCLYKIKSDGKLYOGFNVS 180
 OY 181 VOGIIIVRAAYFGIYDTAKGMLPDPKNTHTIVSMIAQVTVAAGLTSPEDTVRRMM 240
 DB 181 VOGIIIVRAAYFGIYDTAKGMLPDPKNTHTIVSMIAQVTVAAGLTSPEDTVRRMM 240
 OY 241 OSGRKGTDMVTGTLDCWKRIARDEGSKAFKFGANSNVLRGMGAFVLVLYDEIKY 297
 DB 241 OSGRKGTDMVTGTLDCWKRIARDEGSKAFKFGANSNVLRGMGAFVLVLYDEIKY 297

RESULT 5

O919M9 PRELIMINARY: PRT: 298 AA.

AC O919M9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Adenine nucleotide translocase.
 GN AN1.
 OS *Xenopus laevis* (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; *Xenopus*.
 OX NCBI_TaxID=8353;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
 RT Dynamic Patterns of Expression During Development.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF213147; AAF64471.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mtc_carrier.
 DR InterPro: IPR002030; Mtc_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.

DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 32940 MW: 91B740133751877F CRC64;

Query Match 92.1%; Score 1425; DB 13; Length 298;
 Best Local Similarity 91.6%; Pred. No. 4,5e-118;
 Matches 271; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

OY 1 MTDALSFADKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYKGIIDCVVR 60
 DB 1 MTDALISFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYKGIIDCVVR 60
 OY 61 IPKEDEVLSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLGVDKRTQFWRPAGNLASG 120
 DB 61 IPKEGDFVSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLGVDKRTQFWRPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFAPTRLAADYKAGAREFRGLGDCLYKIKSDGKLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFAPTRLAADYKAGAREFRGLGDCLYKIKSDGKLYOGFNVS 180
 OY 181 VOGIIIVRAAYFGIYDTAKGMLPDPKNTHTIVSMIAQVTVAAGLTSPEDTVRRMM 240
 DB 181 VOGIIIVRAAYFGIYDTAKGMLPDPKNTHTIVSMIAQVTVAAGLTSPEDTVRRMM 240
 OY 241 OSGRKGTDMVTGTLDCWKRIARDEGSKAFKFGANSNVLRGMGAFVLVLYDEIKY 296
 DB 241 OSGRKGTDMVTGTLDCWKRIARDEGSKAFKFGANSNVLRGMGAFVLVLYDEIKY 296

RESULT 6

O46373 PRELIMINARY: PRT: 298 AA.

AC O46373;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS *Oryctolagus cuniculus* (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKLETTAL MUSCLE;
 RA Yamaguchi N., Kasai M.;
 RT "Identification of a 30kDa calsequestrin-binding protein, which
 RT regulates calcium release from sarcoplasmic reticulum of rabbit
 RT skeletal muscle.";
 RL J. Biochem. 335:541-547(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB009386; BAA23777.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mtc_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 32901 MW: CAEA32C88164AD78 CRC64;

Query Match 92.0%; Score 1423; DB 6; Length 298;
 Best Local Similarity 89.9%; Pred. No. 6,8e-118;
 Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

OY 1 MTDALSFADKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYKGIIDCVVR 60
 DB 1 MSDQALSFADKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYKGIIDCVVR 60
 OY 61 IPKEDEVLSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLGVDKRTQFWRPAGNLASG 120
 DB 61 IPKEGDFVSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLGVDKRTQFWRPAGNLASG 120


```

DB 181 VGGIITIRRAVGIYDTAKGMLPDPKNTHTFVSMIAQSVTAAGSGTPEFTVRRMM 240
OY 241 QSGRKGDTIMYTGTLDCWKRIARDEGKAFFK 272
    ||||| :|||:|||||:|||||:
DB 241 QSGRKAELIMYSGTIDCWKKIARDEGKAFFR 272

RESULT 9
O95VX4 PRELIMINARY: PRT; 299 AA.
AC O95VX4:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE ADP-ATP translocator.
OS Ethmostigmus rubripes.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda; Chilopoda;
OC Pleurostomophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
OX NCBI_TaxId=62613;
RN [1]
RP SEQUENCE FROM N.A.
RA Burrell J.N.;
RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
RT rubripes."
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF401758; AL02100.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carf.3.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SQ SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C5C5E CRC64;

Query Match 82.6%; Score 1278; DB 5; Length 299;
Best Local Similarity 82.8%; Pred. No. 4,7e-105;
Matches 241; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

OY 5 ALSFAKDFLAGVAAIASTAVAPIERVKLLLOVHASKOITADKOYKGIICVVRIPKE 64
DB 5 AVSFLKDFLAGVAAIAISTVAPIERVKLLLOVHASKOITADKOYKGVDCFVARIPOE 64
OY 65 QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLSGAAG 124
DB 65 QGILSYWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLSGAAG 124
OY 125 ATSLCFVYPLDFAKRIADLVGKAGAEFRGIGDCLVITYKSDGKIGLYOGFNVSVOGI 184
DB 125 ATSLCFVYPLDFAKRIADLVGKAGAEFRGIGDCLVITYKSDGKIGLYOGFNVSVOGI 184
OY 185 IYRAAYFGIYDTAKGMLPDPKNTHTFVSMIAQSVTAAGSLTYPEDTVRRMMQSGR 244
DB 185 IYRAAYFGIYDTAKGMLPDPKNTHTFVSMIAQSVTAAGSLTYPEDTVRRMMQSGR 244
OY 245 KGTIDIMYTGTLDCWKRIARDEGKAFFKGAWSNVLRGMGAFLVLYDEIK 295
DB 245 KADILYKNTIDCWKRIYKTEGGAFFKGAWSNVLRGMGAFLVLYDEIK 295

RESULT 10
O95S30 PRELIMINARY: PRT; 299 AA.
AC O95S30:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE GMI2886P (LP02726P).
GN SE5B OR CG16944.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydrioides; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RA Stapleton M., Brokstein P., Hong L., Agbayanl A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guanin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.

[12]
RN SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayanl A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guanin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuncio J., Pacle J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY060978; AAL28526.1; -.
DR EMBL; AY070894; AAL48516.1; -.
DR FlyBase; FBgn003360; se5B.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carf.3.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_3.
SQ SEQUENCE 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;

Query Match 81.0%; Score 1253.5; DB 5; Length 299;
Best Local Similarity 81.2%; Pred. No. 6,9e-103;
Matches 237; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

OY 5 ALSFAKDFLAGVAAIASTAVAPIERVKLLLOVHASKOITADKOYKGIICVVRIPKE 64
DB 7 AVGFVDFAGAGISAAVSKTAAPIRVKLLLOVHAIHQISIDKQYKGVDCFTIRIPE 66
OY 65 QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLSGAAG 124
DB 67 QGGSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLSGAAG 126
OY 125 ATSLCFVYPLDFAKRIADLVGKAGAEFRGIGDCLVITYKSDGKIGLYOGFNVSVOGI 184
DB 127 ATSLCFVYPLDFAKRIADLVGKAGAEFRGIGDCLVITYKSDGKIGLYOGFNVSVOGI 185
OY 185 IYRAAYFGIYDTAKGMLPDPKNTHTFVSMIAQSVTAAGSLTYPEDTVRRMMQSGR 244
DB 186 IYRAAYFGIYDTAKGMLPDPKNTHTFVSMIAQSVTAAGSLTYPEDTVRRMMQSGR 245
OY 245 KGTIDIMYTGTLDCWKRIARDEGKAFFKGAWSNVLRGMGAFLVLYDEIK 296
DB 246 KATEVIYKNTLHCWATIAKQEGTGAFFKGAWSNVLRGMGAFLVLYDEIK 297

RESULT 11
O9NHM5 PRELIMINARY: PRT; 300 AA.
AC O9NHM5:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE ADP/ATP translocase.
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestrioides; Calliphoridae; Lucilia.
OX NCBI_TaxId=7375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SS MAL SEEKING;
RA Chen Z., Pair J.A., Batterham P.;
RT "A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina."
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL.
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF218587; AAF33322.1; -.
DR InterPro; IPR001993; Mitoch_carrier.

```


RESULT 14
 Q25129 PRELIMINARY: PRT: 304 AA.
 AC Q25129;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 GN HRA7L1.
 OS Halocynthia roretzi (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyuridae; Halocynthia.
 OX NCBI_TaxID=7729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miya T.;
 RL Submitted (Jan-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Miya T.;
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Miya T., Makebe K., Satoh N.;
 RT "Expression of a gene for major mitochondrial protein, ADP/ATP translocase, during embryogenesis in the ascidian Halocynthia roretzi."
 RT roretzi."
 RL Dev. Growth Differ. 36:39-48(1994).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: D83069; BA01765.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carrier. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER. 3.
 DR Inner membrane; Mitochondrion; Transmembrane; Transport.
 KW SEQUENCE 304 AA; 33307 MW; 51FDD07D6B654880 CRC64;
 SQ
 Query Match 74.0%; Score 1145.5; DB 5; Length 304;
 Best Local Similarity 75.4%; Pred. No. 2.6e-93;
 Matches 221; Conservative 21; Mismatches 50; Indels 1; Gaps 1;
 QY 4 AALSAKFLAGVAAISKTAVADIERVKLLQVOHASKQITADKQYKGIIDCVVRIPK 63
 DB 4 SAVDEAKLAIIGCTAAAIKSTIVADIERVKLLQVOAVSTQKAGTEYKGIIDAFVRIPK 63
 QY 64 EOEVLSPFRGNLANIYRFPQALNFAFRDKKQIFLGVDKRTQFWRFAFNLASGGA 123
 DB 64 EGGFSLMRGNLANIYRFPQALNFAFRDKKQIFLGVDKRTQFWRFAFNLASGGA 123
 QY 124 GATSLCFVYPLDFARTRLAADYGKAGAREFRGLDCLVKIKYKSGIKGLYGGFNVSYOG 183
 DB 124 GATGCLCFVYPLDFARTRLAADYG-SGGSKQFTGLGNCLATIYKKDQPRGLYGGFNVSYOG 182
 QY 184 IIVYRAAVFGIYDTAKGMLPDKRNTIYVSNMIAQTVTAVALGTSYPPEDTVRRMMOSG 243
 DB 184 IIVYRAAVFGIYDTAKGMLPDKRNTIYVSNMIAQTVTAVALGTSYPPEDTVRRMMOSG 242
 QY 244 RKGDTIMVTGTDCKRKRLARDGKAFKFGKANSVLKRGKGFVLYLDEIKK 296
 DB 244 RKKEDRMVKYGVDCWKIYKNEGKAFKFGKALSNVIRGTGALVLYLDELKK 295
 RESULT 15
 Q62526 PRELIMINARY: PRT: 307 AA.
 AC Q62526;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ANT2 protein.
 GN ANT2 OR C61663.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champs M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.P., Bouck J., Brokstein P., Brotlier P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegyan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 RA Palazolo M., Peltman G.S., Pan S., Pollard J.P., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkas R., Tector C., Turner R., Venter L., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenhach J.,
 RA Williams S.M., Woodage T., Wortley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OREGON-R;
 RA Zhang Y.Q., Davis A.W., Roote J., Ashburner M.;
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003484; AAF47956.1;
 DR EMBL: Y10618; CAH71629.1;
 DR Flybase: FBgn0025111; Ant2.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carrier. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER. UNKNOWN 2.
 SQ SEQUENCE 307 AA; 33744 MW; 3D6B3D0F8D8061C0C CRC64;
 Query Match 72.8%; Score 1125.5; DB 5; Length 307;
 Best Local Similarity 73.9%; Pred. No. 1.5e-91;
 Matches 215; Conservative 27; Mismatches 46; Indels 1; Gaps 1;
 QY 7 SFAKDFLAGVAAISKTAVADIERVKLLQVOHASKQITADKQYKGIIDCVVRIPK 66
 DB 17 SFLMPFMGVSAAIAKTAIVADIERVKLLQVOEVSQITADKQYKGIIDCVVRIPK 76
 QY 67 VLSFMRGNLANIYRFPQALNFAFRDKKQIFLGVDKRTQFWRFAFNLASGGAAGT 126
 DB 77 ESSFMRGNLANIYRFPQALNFAFRDKKQIFLGVDKRTQFWRFAFNLASGGAAGT 136
 QY 127 SLCFVYPLDFARTRLAADYGKAGAREFRGLDCLVKIKYKSGIKGLYGGFNVSYOGIIT 186
 DB 127 SLCFVYPLDFARTRLAADYGKAGAREFRGLDCLVKIKYKSGIKGLYGGFNVSYOGIIT 186

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd

Om protein - protein search, using sw model

Run on: November 12, 2002, 16:42:45 ; Search time 30.0336 Seconds

Title: US-09-393-441-33
 Perfect score: 1543
 Sequence: 1 MTEQAISFAKDFLAGGIAA.....LRGMGAFFVLYDELKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 9084700

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database : **A_Gensedb.010002.***

1:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1543	100.0	298	21	AAV71033	Human adenine nucleotide
2	1543	100.0	298	22	AAAG39641	Human polypeptide
3	1543	100.0	298	22	AAU103200	Human adenine nucleotide
4	1543	100.0	298	23	AAU103380	Human adenine nucleotide
5	1543	100.0	323	22	AAAG41427	Human polypeptide
6	1454	94.2	298	21	AAV71032	Human adenine nucleotide
7	1454	94.2	298	22	AAU01199	Human adenine nucleotide
8	1454	94.2	298	23	AAU10379	Human adenine nucleotide
9	1412	91.5	298	19	AAAG61169	Human protein
10	1385.5	89.8	297	21	AAV71031	Human adenine nucleotide

11	1385.5	89.8	297	22	AAU0138
12	1385.5	89.8	297	22	AAU10378
13	1367.5	88.6	325	22	ABG15423
14	1288	81.3	293	22	ABG27056
15	1254.5	81.3	299	22	ABBB6082
16	1254.5	81.3	307	22	ABBB7300
17	1137.5	73.7	297	22	ABBB8360
18	1119	72.5	315	23	AAE21175
19	1044	67.5	328	23	ABPA3205
20	879.5	57.0	298	22	ABG18922
21	763	49.4	484	22	ABG15422
22	763	49.4	484	22	ABG27055
23	749.5	48.6	386	22	AAAM0106
24	742.5	48.1	346	21	AAAG36577
25	742.5	48.1	346	21	AAAG37261
26	742.5	48.1	346	21	AAAG37264
27	742.5	48.1	346	21	AAAG38460
28	742.5	48.1	346	21	AAAG38460
29	742.5	48.1	363	21	AAAG36576
30	742.5	48.1	363	21	AAAG37263
31	742.5	48.1	363	21	AAAG38459
32	742.5	48.1	381	21	AAAG36575
33	742.5	48.1	381	21	AAAG37259
34	742.5	48.1	381	21	AAAG37262
35	742.5	48.1	381	21	AAAG38458
36	742.5	48.1	922	21	AAAG38672
37	742.5	48.1	1009	21	AAAG38671
38	742.5	48.1	1027	21	AAAG38670
39	739.5	47.9	346	21	AAAG17731
40	739.5	47.9	363	21	AAAG17730
41	739.5	44.7	381	21	AAAG17729
42	688.5	44.6	330	21	AAAG30658
43	688.5	44.6	330	21	AAAG39389
44	679.5	44.0	333	21	AAAG68857
45	679.5	44.0	330	21	AAAG68856

ALIGNMENTS

RESULT 1	
AAV71033	
ID	AAV71033 standard; Protein; 298 AA.
XX	
AC	AAV71033;
XX	
DT	29-AUG-2000 (first entry)
XX	
DE	Human adenine nucleotide translocator ANT3.
XX	
XX	Human: adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW	mitochondrial permeability transition; neuroprotective; neurotropic;
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	antiparalytic; cerebroprotective; therapeutic; screening; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia
KW	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
XX	
OS	Homo sapiens.
XX	
PN	W0200026370-A2.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-US25883.
XX	
PR	03-NOV-1998; 98US-0185904.
PR	08-SEP-1999; 99US-0393441.
XX	
PA	(MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 XX
 DR WPI: 2000-365619/31.
 DR N-PSDB: AAD00521.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 PS
 PS Claim 46: Page 173-174; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MID), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 CC
 XX
 SQ Sequence 298 AA;
 XX
 Query Match 100.0%; Score 1543; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4, 8e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQAISFADFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIADKQYKGIIVDCIVR 60
 Db 1 MTEQAISFADFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIADKQYKGIIVDCIVR 60
 QY 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHHQFWRFFAGNLASG 120
 Db 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHHQFWRFFAGNLASG 120
 QY 121 GAAGATSLCFYPLDFARTRLAADVGSCTFERERGLDCLVTKTSDGIRGLYQGSFVS 180
 Db 121 GAAGATSLCFYPLDFARTRLAADVGSCTFERERGLDCLVTKTSDGIRGLYQGSFVS 180
 QY 181 VQGIITIRAAVFGYVDFAKGLPDPKNTHTIVSMIAQTVAAGVVSYPEDTVRRRMM 240
 Db 181 VQGIITIRAAVFGYVDFAKGLPDPKNTHTIVSMIAQTVAAGVVSYPEDTVRRRMM 240
 QY 241 QSGRRKADIMYTGTCWRKIFRDEGGAFFKAGMSNVLRMGAFVLYLYDELKVI 298
 Db 241 QSGRRKADIMYTGTCWRKIFRDEGGAFFKAGMSNVLRMGAFVLYLYDELKVI 298
 RESULT 2
 AAM39641
 ID AAM39641 standard; Protein: 298 AA.
 XX
 AC AAM39641;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2786.
 XX
 KW Human: nootropic; immunosuppressant; cytosstatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KM Leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000MO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AAI58797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 PS
 PS Example 4: SEQ ID NO 2786; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytosstatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 298 AA;
 XX
 Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4, 8e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQAISFADFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIADKQYKGIIVDCIVR 60
 Db 1 MTEQAISFADFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIADKQYKGIIVDCIVR 60
 QY 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHHQFWRFFAGNLASG 120
 Db 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHHQFWRFFAGNLASG 120
 QY 121 GAAGATSLCFYPLDFARTRLAADVGSCTFERERGLDCLVTKTSDGIRGLYQGSFVS 180
 Db 121 GAAGATSLCFYPLDFARTRLAADVGSCTFERERGLDCLVTKTSDGIRGLYQGSFVS 180
 QY 181 VQGIITIRAAVFGYVDFAKGLPDPKNTHTIVSMIAQTVAAGVVSYPEDTVRRRMM 240
 Db 181 VQGIITIRAAVFGYVDFAKGLPDPKNTHTIVSMIAQTVAAGVVSYPEDTVRRRMM 240
 QY 241 QSGRRKADIMYTGTCWRKIFRDEGGAFFKAGMSNVLRMGAFVLYLYDELKVI 298

```

Db      241 OSGRKGADIMYGTVDCKRKIFRDEGKAFFKGAMSNVLRGGAFFVLVYDELKKVI 298
|||||
RESULT 3
AAU01200
ID      AAU01200 standard; Protein: 298 AA.
XX
XX
AC      AAU01200;
XX
XX      07-SEP-2001 (first entry)
DE      Human adenine nucleotide translocator-3 (ANT-3) protein.
XX
XX      Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
KM      mitochondrial permeability transition pore component; cell survival;
KM      mitochondrial core component; mitochondrial related disorder; cancer;
KM      Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX
XX      Homo sapiens.
OS
XX      WO200132876-A2.
XX
XX      10-MAY-2001.
XX
XX      03-NOV-2000; 2000WO-US30535.
XX
XX      03-NOV-1999; 99US-0434354.
PR
XX      (MITO-) MITOKOR.
PA
XX      Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
PI      Vellicelebl G, Davis RE;
DR      MPI; 2001-291054/30.
DR      N-PSDB; AAS05903.
XX
XX      New nucleic acid expression constructs, useful for screening for agents
PT      that alter mitochondrial permeability transition (MPT), comprises
PT      polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT      fused to energy transfer molecule -
XX
XX      Disclosure: Fig 2; 186pp; English.
PS
XX
XX      The present sequence represents human adenine nucleotide translocator-3
CC      (ANT-3) protein. ANT proteins are mitochondrial permeability
CC      transition (MPT) pore components responsible for mediating transport
CC      of ADP across the mitochondrial inner membrane. ANT proteins interact
CC      with other mitochondrial core components e.g. cyclophilins to
CC      regulate MPT. The present invention relates to a novel nucleic acid
CC      expression construct comprising a promoter operably linked to a
CC      polynucleotide encoding a mitochondrial pore component polypeptide
CC      (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC      (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC      expression construct can alter mitochondrial membrane permeability
CC      transition and/or alter the interaction between mitochondrial core
CC      components. The methods are useful for screening for agents that alter
CC      MPT and/or cell survival. These agents are useful for the prevention or
CC      treatment of diseases associated with altered mitochondrial function or
CC      dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC      mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC      mitochondrial encephalopathy, lactic acidosis, stroke,
CC      hyperproliferative disorders e.g. cancer, and deafness.
XX
XX      Sequence 298 AA:
SQ
Query Match      100.0%; Score 1543; DB 22; Length 298;
Best Local Similarity 100.0%; Pred. No. 4,8e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      61 IPKEGCVSEFWGKNLANVIRPEPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
|||||
Db      61 IPKEGCVSEFWGKNLANVIRPEPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
Oy      121 GAAGATSLCFYVPLDPFARTRLAADVKGSTEEFEGLDCLVTKRSDGIRLTYGFSYS 180
|||||
Db      121 GAAGATSLCFYVPLDPFARTRLAADVKGSTEEFEGLDCLVTKRSDGIRLTYGFSYS 180
Oy      181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVTAVAGVSYPEPTVRRMM 240
|||||
Db      181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVTAVAGVSYPEPTVRRMM 240
Oy      241 OSGRKGADIMYGTVDCKRKIFRDEGKAFFKGAMSNVLRGGAFFVLVYDELKKVI 298
|||||
Db      241 OSGRKGADIMYGTVDCKRKIFRDEGKAFFKGAMSNVLRGGAFFVLVYDELKKVI 298
|||||
RESULT 4
AAU10380
ID      AAU10380 standard; Protein: 298 AA.
XX
XX      AAU10380;
XX
XX      14-FEB-2002 (first entry)
DE      Human adenine nucleotide translocator 3 (ANT3).
XX
XX      Human; adenine nucleotide translocator; ANT;
KM      mitochondrial matrix protein.
XX
XX      Homo sapiens.
OS
XX      WO200185944-A2.
XX
XX      15-NOV-2001.
XX
XX      11-MAY-2001; 2001WO-US15416.
XX
XX      11-MAY-2000; 2000US-0569327.
PR
XX      (MITO-) MITOKOR.
PA
XX      Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI      Ghosh SS, Moos WH, Pel Y, Carroll AK;
DR      MPI; 2002-055598/07.
DR      N-PSDB; AAS16690.
XX
XX      Novel recombinant expression construct for producing adenine nucleotide
PT      translocator polypeptides, comprises a regulated promoter linked to
PT      nucleic acid encoding the polypeptide -
XX
XX      Example 3: Fig 2; 147pp; English.
PS
XX
XX      The invention relates to a recombinant expression construct (1)
CC      comprising a regulated promoter operably linked to a nucleic acid
CC      encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC      proteins mediate the exchange of ATP synthesised in the mitochondrial
CC      matrix for ADP in the cytosol. (1) is useful for producing recombinant
CC      ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC      culturing the host cell. (1) is also useful for targeting a polypeptide
CC      of interest to a mitochondrial membrane, where ANT polypeptide is
CC      expressed as a fusion protein with the polypeptide of interest.
CC      Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC      useful for identifying an agent that binds to an ANT polypeptide. ANT
CC      ligand is useful for determining the presence of an ANT polypeptide,
CC      preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC      ANT from a biological sample, where the ANT ligand is covalently or non-
CC      covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC      useful for identifying an agent that interacts with an ANT polypeptide.
XX      The present sequence represents the amino acid sequence of human ANT3.
XX

```

SQ Sequence 298 AA: Query Match 100.0%; Score 1543; DB 23; Length 298; Best Local Similarity 100.0%; Pred. No. 4,8e-157; Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQALSFADFLAGGIAAISKTAAPIERVKLLQVHASKQIADKQKGIIVDCIVR 60
 DB 1 MTEQALSFADFLAGGIAAISKTAAPIERVKLLQVHASKQIADKQKGIIVDCIVR 60

QY 61 IPKQGLSWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLASG 120
 DB 61 IPKQGLSWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRLADVGSCTEREFRGLGDLVTKITKSDGIRGLYQGSFVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGSCTEREFRGLGDLVTKITKSDGIRGLYQGSFVS 180

QY 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSMMIAQVTAAGVSYPPDVTYRRMM 240
 DB 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSMMIAQVTAAGVSYPPDVTYRRMM 240

QY 241 QSGRRKADIMYTGTVDCWRKIFRDEGKAFKFGAMSNVLKMGAFVLYLYDELKVI 298
 DB 241 QSGRRKADIMYTGTVDCWRKIFRDEGKAFKFGAMSNVLKMGAFVLYLYDELKVI 298

RESULT 5
 AAM41427 standard; Protein; 323 AA.

XX ID AAM41427
 XX AC AAM41427;
 XX DT 22-OCT-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 6358.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemokine;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.
 OS
 XX
 PN WO200153312-A1.
 PD 26-JUL-2001.
 XX 26-DEC-2000; 2000MO-US34263.
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.
 PA
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 DR N-PSDB; AAI60583.
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX

PS Example 2; SEQ ID NO 6358; 10078bp; English.
 XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

SQ Sequence 323 AA: Query Match 100.0%; Score 1543; DB 22; Length 323; Best Local Similarity 100.0%; Pred. No. 5,4e-157; Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQALSFADFLAGGIAAISKTAAPIERVKLLQVHASKQIADKQKGIIVDCIVR 60
 DB 26 MTEQALSFADFLAGGIAAISKTAAPIERVKLLQVHASKQIADKQKGIIVDCIVR 85

QY 61 IPKQGLSWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLASG 120
 DB 86 IPKQGLSWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLASG 145

QY 121 GAAGATSLCFVYPLDFARTRLADVGSCTEREFRGLGDLVTKITKSDGIRGLYQGSFVS 180
 DB 146 GAAGATSLCFVYPLDFARTRLADVGSCTEREFRGLGDLVTKITKSDGIRGLYQGSFVS 205

QY 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSMMIAQVTAAGVSYPPDVTYRRMM 240
 DB 206 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSMMIAQVTAAGVSYPPDVTYRRMM 265

QY 241 QSGRRKADIMYTGTVDCWRKIFRDEGKAFKFGAMSNVLKMGAFVLYLYDELKVI 298
 DB 266 QSGRRKADIMYTGTVDCWRKIFRDEGKAFKFGAMSNVLKMGAFVLYLYDELKVI 323

RESULT 6
 AAY71032 standard; Protein; 298 AA.

XX ID AAY71032
 XX AC AAY71032;
 XX DT 29-AUG-2000 (first entry)
 XX Human adenine nucleotide translocator ANT2.
 DE
 XX Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; nootropic;
 KW antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic;
 KW antipsoriatic; cerebroprotective; therapeutic; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIPD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.
 OS
 XX
 PN WO200026370-A2.
 PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-US25883.
XX
PR 03-NOV-1998; 98US-0185904.
PR 08-SEP-1999; 99US-0393441.
XX
PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SM, Szabo TR;
PI Ghosh SS;
DR WPI: 2000-365619/31.
DR N-PSDB: AAD00520.
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease
XX
PS Claim 45; Page 172-173; 175pp; English.
XX
CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC d1/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT2 from human brain.
XX
SQ Sequence 298 AA:

Query Match 94.2%; Score 1454; DB 21; Length 298;
Best local Similarity 92.6%; Pred. No. 1.7e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQATSFANDFLAGGAAIAISKTAAPIERVKLLQOVHASKQIADKQKGIIVDCIVR 60
DB 1 MTEAALSFADFLAGGAAIAISKTAAPIERVKLLQOVHASKQIADKQKGIIVDCIVR 60
QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLIASG 120
DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLIASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGKSTGERFRGLGDCLVKTKSDGIRGLYQGFVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGKSTGERFRGLGDCLVKTKSDGIRGLYQGFVS 180
QY 181 VOGIITIRAAVFGVYDTAKMLPDPKNTHTIVSMIAQTAVAGVSYFPDVRRRMM 240
DB 181 VOGIITIRAAVFGVYDTAKMLPDPKNTHTIVSMIAQTAVAGVSYFPDVRRRMM 240
QY 241 QSGRKADIMVTGTVDCKWRKIFRDEGGKAFKGAWSNVLRGMGAFLVLYDELK 296
DB 241 QSGRKADIMVTGTVDCKWRKIFRDEGGKAFKGAWSNVLRGMGAFLVLYDELK 296

RESULT 7
AAU01199
ID AAU01199 standard; Protein; 298 AA.
XX
AC AAU01199;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human adenine nucleotide translocator-2 (ANT-2) protein.

XX
KW Human: adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX
OS Homo sapiens.
XX
PN WO200132876-A2.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-US30535.
PR 03-NOV-1999; 99US-0434354.
XX
PA (MITO-) MITOKOR.
XX
PI Murphy AN, Clevenger W, Willey SE, Andreyev AV, Fritger LG;
PI Vellelebi G, Davis RE;
DR WPI: 2001-291054/30.
DR N-PSDB: AAS05902.
XX
PT New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
PS Disclosure; Fig 2; 166pp; English.
XX
CC The present sequence represents human adenine nucleotide translocator-2
CC (ANT-2) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke, schizophrenia,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ Sequence 298 AA:

Query Match 94.2%; Score 1454; DB 22; Length 298;
Best local Similarity 92.6%; Pred. No. 1.7e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQATSFANDFLAGGAAIAISKTAAPIERVKLLQOVHASKQIADKQKGIIVDCIVR 60
DB 1 MTEAALSFADFLAGGAAIAISKTAAPIERVKLLQOVHASKQIADKQKGIIVDCIVR 60
QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLIASG 120
DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLIASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGKSTGERFRGLGDCLVKTKSDGIRGLYQGFVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGKSTGERFRGLGDCLVKTKSDGIRGLYQGFVS 180
QY 181 VOGIITIRAAVFGVYDTAKMLPDPKNTHTIVSMIAQTAVAGVSYFPDVRRRMM 240
DB 181 VOGIITIRAAVFGVYDTAKMLPDPKNTHTIVSMIAQTAVAGVSYFPDVRRRMM 240

CC Inner mitochondrial membrane. It mediates transport of adenosine

DR N-PSDB; AAS05901.

XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT.
XX WPI: 2001-639362/73.
XX N-PSDB; AAS79610.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 45782; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 325 AA:
SQ
Query Match 88.6%; Score 1367.5; DB 22; Length 325;
Best Local Similarity 88.0%; Pred. No. 3.8e-138;
Matches 263; Conservative 13; Mismatches 20; Indels 3; Gaps 2;
QY 1 MTEQAISFANDFLAGTAAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIVDCIVR 60
DB 24 MTEAANVSFADFLAGVAAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIVDCIVR 83
QY 61 IPKEQGLSWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHNQFMRFGANLASG 120
DB 84 IPKEQGLSWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHNQFMRFGANLASG 143
QY 121 GAAGATSLCEVYPLDFARTRLADVGKSTEREFGDGLVTKKSDGINTGQGSFVS 180
DB 144 GAAGATSLCEVYPLDFARTRLADVGKATEREFGDGLVTKKSDGINTGQGSFVS 203
QY 181 VOGIITRAAYFGYDTAKGMLPDKFTHYVSMIAQTV-TAAVAGVSTPFDT--VRRR 237
DB 204 VOGIITRAAYFGYDTAKGMLPDKFTHYVSMIAQTVHCCGCCGLPYFPFDRSVARN 263

QY 238 MMOSGRKADIMYGTGVDCKRIERDEGKAFPEKGAWSNVLRMGSAFVLYLDELKK 296
DB 264 EXMOSGRKGYDIMGYTLGDCMRKIAERDEGKAFPEKGAWSNVLRMGSAFVLYLDELKK 322
RESULT 14
ID ABG27056 standard; Protein; 263 AA.
AC ABG27056;
DT 18-FEB-2002 (first entry)
DE Novel human diagnostic protein #27047.
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT.
XX WPI: 2001-639362/73.
XX N-PSDB; AAS91243.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 57415; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 263 AA:
SQ
Query Match 83.5%; Score 1288; DB 22; Length 263;
Best Local Similarity 92.7%; Pred. No. 9.6e-130;
Matches 242; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
QY 1 MTEQAISFANDFLAGTAAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIVDCIVR 60
DB 24 MTEAANVSFADFLAGVAAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIVDCIVR 83

Db 1 MTDAVSAKDFLAGGVAASIKSTAVAPIERVKLLLOVQHASKOITPADKQYKGIIDCVVR 60
Qy 61 IPKEGVSLFPMRGNLANVIRYPTQALNFAFKDKYKQJFLGVDKHTQFWRYPAGNLASG 120
Db 61 IPKEGVSLFPMRGNLANVIRYPTQALNFAFKDKYKQJFLGVDKHTQFWRYPAGNLASG 120
Qy 121 GAAGATSLCFYVPLDFAFTRLAADYKSGTEREPRGLDCLVKIRKSDGIRGLYOGFSYS 180
Db 121 GAAGATSLCFYVPLDFAFTRLAADYKSGTEREPRGLDCLVKIRKSDGIRGLYOGFSYS 180
Qy 181 VOGIITVAAAFGVYDTAKGMLPDPKNTHIYVSMIAQTVAVAGVSYPTVRRMM 240
Db 181 VOGIITVAAAFGVYDTAKGMLPDPKNTHIYVSMIAQTVAVAGVSYPTVRRMM 240
Qy 241 QSGRKADIMYTGIVDCWKRI 261
Db 241 QSGRKGTDMYTGITDCWKRI 261

RESULT 15

ABB66082
ID ABB66082 standard; Protein; 299 AA.

AC ABB66082;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 25038.

KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PSDB; ABL10185.

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

PS Disclosure; SEQ ID NO 25038; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins (AB16173-AB16172).
CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 299 AA;

Qy 5 AISEAKDFLAGGIAAASIKSTAVAPIERVKLLLOVQHASKOIAADKQYKGIYDCIVRIPE 64
Db 7 AVGFYKDEFAAGISAAVSKTAVAPIERVKLLLOVQHISKQISPKQYGMWDCFIRIPE 66
Qy 65 QGVLSFMRGNLANVIRYPTQALNFAFKDKYKQJFLGVDKHTQFWRYPAGNLASGGAAG 124
Db 67 QGVLSFMRGNLANVIRYPTQALNFAFKDKYKQJFLGVDKHTQFWRYPAGNLASGGAAG 126
Qy 125 ATSLCFYVPLDFAFTRLAADYKSGTEREPRGLDCLVKIRKSDGIRGLYOGFSYSVOCI 184
Db 127 ATSLCFYVPLDFAFTRLAADYKSGTEREPRGLDCLVKIRKSDGIRGLYOGFSYSVOCI 185
Qy 185 IYRAAYFGVYDTAKGMLPDPKNTHIYVSMIAQTVAVAGVSYPTVRRMMQSGR 244
Db 186 IYRAAYFGVYDTAKGMLPDPKNTPIYISMAIAQVTVAVAGVSYPTVRRMMQSGR 245
Qy 245 KGADIMYTGIVDCWKRIFRDEGSKAFKFGANSNVLKRGKAFVLVLYDELKVI 298
Db 246 KATEVIYKNTLHCWMTIAKQEGTGAFFKGAFAFSNLLRGTAFAVLVLYDEIKKVL 299

Search completed: November 12, 2002, 16:45:58
Job time : 31.0336 secs

Query Match 81.3%; Score 1254.5; DB 22; Length 299;
Best Local Similarity 80.6%; Pred. No. 4.5e-126;
Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:25 ; Search time 11.6797 Seconds
(without alignments)
750.705 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MTEQAISFAKDFLAGIAA.....LRGMGAFLVLYDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfillsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1412	91.5	298	3	US-08-961-871-10 Sequence 10, Appl
2	311	20.2	469	4	US-09-188-930-339 Sequence 339, App
3	283.5	18.4	291	4	US-09-501-558-2 Sequence 2, Appl1
4	280	18.1	447	4	US-09-160-119-4 Sequence 4, Appl1
5	280	18.1	674	4	US-09-160-119-2 Sequence 2, Appl1
6	265	17.2	312	4	US-09-142-565-2 Sequence 2, Appl1
7	250.5	16.2	299	1	US-08-518-878-56 Sequence 56, Appl
8	250.5	16.2	299	2	US-08-470-868A-56 Sequence 56, Appl
9	250.5	16.2	309	1	US-08-518-878B-51 Sequence 51, Appl
10	250.5	16.2	309	2	US-08-807-861A-51 Sequence 51, Appl
11	250.5	16.2	309	3	US-08-470-868A-51 Sequence 51, Appl
12	250.5	16.2	309	3	US-09-210-681-51 Sequence 51, Appl
13	250.5	16.2	309	3	US-08-946-719A-51 Sequence 51, Appl
14	250.5	16.2	311	2	US-08-775-009-33 Sequence 33, Appl
15	245	15.9	432	2	US-08-937-466-4 Sequence 4, Appl1
16	245	15.9	432	2	US-09-172-528-4 Sequence 4, Appl1
17	245	15.9	432	2	US-09-318-199-4 Sequence 4, Appl1
18	245	15.9	432	4	US-09-503-579-4 Sequence 4, Appl1
19	244	15.8	308	2	US-08-937-466-2 Sequence 2, Appl1
20	244	15.8	308	2	US-09-172-528-2 Sequence 2, Appl1
21	244	15.8	308	3	US-09-318-199-2 Sequence 2, Appl1
22	244	15.8	308	4	US-09-503-579-2 Sequence 2, Appl1
23	243.5	15.8	311	2	US-08-775-009-32 Sequence 32, Appl
24	232.5	15.1	320	2	US-08-933-750C-12 Sequence 12, Appl
25	232.5	15.1	320	4	US-09-234-613-12 Sequence 12, Appl
26	227.5	14.7	303	1	US-08-294-522B-36 Sequence 36, Appl
27	226.5	14.7	303	1	US-08-518-878B-37 Sequence 37, Appl

28	226.5	14.7	303	2	US-08-807-861A-37 Sequence 37, Appl
29	226.5	14.7	303	2	US-08-470-868A-37 Sequence 37, Appl
30	226.5	14.7	303	3	US-09-210-681-37 Sequence 37, Appl
31	226.5	14.7	303	3	US-08-946-719A-37 Sequence 37, Appl
32	222	14.4	293	4	US-09-501-558-4 Sequence 4, Appl1
33	211	13.7	306	5	PCT-US94-09799-1 Sequence 1, Appl1
34	205.5	13.3	307	2	US-08-807-861A-56 Sequence 56, Appl
35	205.5	13.3	307	3	US-09-210-681-56 Sequence 56, Appl
36	205.5	13.3	307	3	US-08-946-719A-56 Sequence 56, Appl
37	198.5	12.9	351	2	US-08-933-750C-19 Sequence 19, Appl
38	198.5	12.9	351	4	US-09-234-613-19 Sequence 19, Appl
39	193	12.5	328	4	US-09-068-140A-15 Sequence 15, Appl
40	191	12.4	256	2	US-08-937-466-6 Sequence 6, Appl1
41	191	12.4	256	2	US-09-172-528-6 Sequence 6, Appl1
42	191	12.4	256	3	US-09-318-199-6 Sequence 6, Appl1
43	191	12.4	256	4	US-09-503-579-6 Sequence 6, Appl1
44	181	11.7	289	4	US-09-068-140A-10 Sequence 10, Appl
45	180.5	11.7	312	4	US-09-188-930-142 Sequence 142, App

ALIGNMENTS

RESULT 1
US-08-961-871-10
; Sequence 10, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: MacGregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; City: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,871
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,017
; FILING DATE: 01-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8089
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-961-871-10

Query Match 91.5%; Score 1412; DB 3; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.2e-151;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
QY 1 MTEQAISFAKDFLAGIAAISKTAIVAPRIERVKLLLVGHASKQIAADKQYKIVDCIVR 60

RESULT 3
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:

Query Match	18.1%;	Score 280;	DB 4;	length 447;
Best Local Similarity	27.1%;	Pred. No. 3.9e-23;		
Matches 80; Conservative	47;	Mismatches 148;	Indels 20;	Gaps 6

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-56

Query Match 16.2%; Score 250.5; DB 1; Length 299;

Best Local Similarity 24.9%; Pred. No. 4.7e-20;
Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGGIAAISKTAVERPIERKLLQVQHASK--QIAADKQYKGIYDCIVRIPEQGV 68
DB 7 FLAGGTAACIADLTLPDFAKVRLOIGESQGPVRAVSAQYGVNGTILTWRTGPR 66
QY 69 SFMGNLANVIRYPTQALNFAFDKTKQIFLGVDKHTQPFWRIFAGNLASGGAAGTSL 128
DB 67 SLYNGLVAAGLORQMSFASVIRGLYDSVKQFYTKG-SEHAS---IGSRLLAGSTTGALAV 121
QY 129 CFVYPLFAPTRLAADGKSGTEREPRGLGDCLVKITKSDIGRLXGFSVVOGIIYR 188
DB 122 AVAOPDVVKYRPOAQ-ARAGGRRYOSTVNAVYTTIAREGFRGLMGTSPNVARNAIVN 180
QY 189 AAYGVYDTAK-----GMLPDPKNTIHVYSWMTAQVTAVAGVSYPFDTVRRMMQS 242
DB 181 CAELVTYDLIKDALLLKANLMTDPLCHFTSAFGAGFCTVIAS---PVDVVKTRYM--- 233
QY 243 GRKADIMYGTVCWKRIPEDEGKAFKFGAMSNVLR-GMGCAFVLYLDELKVI 298
DB 234 --NSALQYSSAGHCALTMLOKEGPRAFYKGFMPFLRLGSMVNVMEVTEQLRAL 288

RESULT 8

US-08-470-868A-56

; Sequence 56, Application US/08470868A
; Patent No. 5861485
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis C.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,868A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-56

Query Match 16.2%; Score 250.5; DB 2; Length 299;

Best Local Similarity 24.9%; Pred. No. 4.7e-20;
Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGGIAAISKTAVERPIERKLLQVQHASK--QIAADKQYKGIYDCIVRIPEQGV 68
DB 7 FLAGGTAACIADLTLPDFAKVRLOIGESQGPVRAVSAQYGVNGTILTWRTGPR 66
QY 69 SFMGNLANVIRYPTQALNFAFDKTKQIFLGVDKHTQPFWRIFAGNLASGGAAGTSL 128
DB 67 SLYNGLVAAGLORQMSFASVIRGLYDSVKQFYTKG-SEHAS---IGSRLLAGSTTGALAV 121
QY 129 CFVYPLFAPTRLAADGKSGTEREPRGLGDCLVKITKSDIGRLXGFSVVOGIIYR 188
DB 122 AVAOPDVVKYRPOAQ-ARAGGRRYOSTVNAVYTTIAREGFRGLMGTSPNVARNAIVN 180
QY 189 AAYGVYDTAK-----GMLPDPKNTIHVYSWMTAQVTAVAGVSYPFDTVRRMMQS 242
DB 181 CAELVTYDLIKDALLLKANLMTDPLCHFTSAFGAGFCTVIAS---PVDVVKTRYM--- 233
QY 243 GRKADIMYGTVCWKRIPEDEGKAFKFGAMSNVLR-GMGCAFVLYLDELKVI 298
DB 234 --NSALQYSSAGHCALTMLOKEGPRAFYKGFMPFLRLGSMVNVMEVTEQLRAL 288

RESULT 9

US-08-518-878B-51

; Sequence 51, Application US/0851878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518,878B
; FILING DATE: 23-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:

```

; SEQUENCE CHARACTERISTICS:
;     LENGTH: 309 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: unknown
;
US-08-518-878B-51

```

Query Match	16.2%;	Score 250.5;	DB 1;	Length 309;
Best Local Similarity	24.9%;	Pred. No. 4.9e-20;		
Matches 74; Conservative	52;	Mismatches 146;	Indels 25;	Gaps 8;

[illegible]

RESULT 10
US-08-807-861A-51
; Sequence 51, Application US/08807861A

```

; SEQUENCE CHARACTERISTICS:
;     LENGTH: 309 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: unknown
;
US-08-807-661A-51

```

Query Match	16.2%;	Score 250.5;	DB 2;	Length 309;
Best Local Similarity	24.9%;	Pred. NO. 4.9e-20;		
Matches 74; Conservative	52;	Mismatches 146;	Indels 25;	Gaps 8;

```

QY 12 FLAGIAAASKTVAPIERKLLLYOVHAK --- QIAADOKYKGYIDCIVIRIPEBGVL 68
Db 17 FLGAGTAAACIADLITFFLDPAKRAVLOIQGSGGCVKATVSAQIRGVAGCTILTWRTGSPR 76
QY 69 SEMRGILANVIYFPTQALNEFAFKDKYKQIFLGVDKHQTFWRYEAGNLASGAAGATSL 128
Db 77 SLYNGVLAGLOROMSFASVIRIGLVDYSKOFETKG -SEHAS --- IGSRLLAGSTTGALAV 131
QY 129 CFVYPLDFARILAADVGSGSTEEFEFGLDCLVKIKKSGDGRGLYOGFVSOGIIYR 168
Db 132 AVAOPDVVKKRFOAQ -ARRGGGRRTOSTYNAKTTIAREEFKRLMGSTSPNVAARNAIVN 190
QY 189 AAYGVYDTAK --- GMLPDPANTHIIVVSMIAQTVAAGVSVXPFTVRRRMQOS 242
Db 191 CAELVTVDLIKDALLKANLMTDLPCHFTSAFGAGFCTVIAS --- PVDVVKTRYM --- 243
QY 243 GRKADIMYIGTUDCMKRIPEDEGKAFFGKANSNVLK -GMGCAFVLVLYIDELKKVI 298
Db 244 - -NSALQOYSSAGCALITMLOKEDEPRAFYGGFMSFLRLSMVNVMPVTVEQLKRAL 298

```

RESULT 11
US-08-470-868A-51
; Sequence 51, Application US/08470868A

```

? INFORMATION FOR SEQ ID NO: 51:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 309 amino acids
?
? type: amino acid
?
? STRANDEDNESS: single
?
? TOPOLOGY: unknown
?
? OS-08-470--8684-51

```


QY 12 FLAGIAAAISKTAVERVKLLQVQHASKQIAADKQYKGI VDCIVRIPKEQVLSFW 71

```
Db 17 FLAGGTACEFADLLTFPLDPAKVRLOIQ-GENPGAOSVOYRGVLGTLITWVRETEGPRSPY 75
QY 72 RGNLANVIRYPPPTQALNPAFMDKXKOJFLGGVDKHTQFMWRYFAGNLSGGAAGATSLCFV 131
Db 76 SGLVAGLHRQMSFASIRIGLYDSVKOFTYFKGADHSS----VAIRILAGCTTGMAAVTCA 131
QY 132 YPLDFAARTRLAADVG-KSGTEREPRGLDCLVKITKSDGIRGLYQGFSSVVOGIIIVRAA 190
Db 132 QPTDVVKKVRFQAMIRLGTGGGERKRYGTMDAYRTIAREGVRGLWKGTWPNITRNAIYNCA 191
QY 191 YFGYYDTAKGMLPDPKNTNHIYVSMIAQTYTA-----VAGVSYTEPDTVRRRAM-MOSGR 244
Db 192 EMVTYDIIKEKLE---SHEFTDNFPCHEVSAFGAGFCATVVASPDVVKTRYMNAPLGR 248
QY 245 KGADIMYTGTVDCWRKIIFRDEGKAFPKGAMSNVLR-GMGCAFVLVLYDELKVTI 298
Db 249 -----YRSPILCHMLKNVAODEGPTAFYKGFVPSFLRLGAMNMMEVITYEQLKRAL 297
```

Search completed: November 12, 2002, 16:49:20
job time : 13.0131 secs

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84


```
Db 1 MTDAAISFAKDFLAGGVAALAAISKTAVAPIERVKLLQVHASKQJIAADKQYKGIIDCVVR 60
Qy 61 IPKEGVLSEFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDNKHQFMRFAGNLSAG 120
Db 61 IPKEGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDNKHQFMRFAGNLSAG 120
Qy 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREPFGDCLVKTIKSGICGLYOGFSVS 180
Db 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREPFGDCLVKTIKSGICGLYOGFSVS 180
Qy 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTIIVSWMIAQTVTAAGVSVSPEDTVRRMM 240
Db 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTIIVSWMIAQTVTAAGVSVSPEDTVRRMM 240
Qy 241 QSGRKGADIMYGTVDCKRKIFRDEGKAFKFGANSNVLRCMGAFVLVYDELK 296
Db 241 QSGRKGADIMYGTVDCKRKIFRDEGKAFKFGANSNVLRCMGAFVLVYDELK 296
```

RESULT 5
US-09-811-094-31

```
; Sequence 31, Application US/09811094
; Patent No. US2001004414A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811.094
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-31
```

Query Match 89.8%; Score 1385.5; DB 10; Length 297;
Best Local Similarity 87.2%; Pred. No. 7.4e-136; Indels 1; Gaps 1;
Matches 260; Conservative 21; Mismatches 16;

```
Qy 1 MTEOAISFAKDFLAGGIAAISKTAVAPIERVKLLQVHASKQJIAADKQYKGIIDCVVR 60
Db 1 MGDHMSFLKDFLAGGVAALAAVSKTAVAPIERVKLLQVHASKQJIAEKQYKGIIDCVVR 60
Qy 61 IPKEGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDNKHQFMRFAGNLSAG 120
Db 61 IPKEGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDNKHQFMRFAGNLSAG 120
Qy 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREPFGDCLVKTIKSGICGLYOGFSVS 180
Db 121 GAAGATSLCFYVPLDFARTRLAADVGR-AGREFHGLDCLIKIKSGICGLYOGFSVS 179
Qy 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTIIVSWMIAQTVTAAGVSVSPEDTVRRMM 240
Db 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTIIVSWMIAQTVTAAGVSVSPEDTVRRMM 239
Qy 241 QSGRKGADIMYGTVDCKRKIFRDEGKAFKFGANSNVLRCMGAFVLVYDELK 298
Db 241 QSGRKGADIMYGTVDCKRKIFRDEGKAFKFGANSNVLRCMGAFVLVYDELK 297
```

RESULT 6

```
US-09-810-644-31
; Sequence 31, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810.644
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-31
```

Query Match 89.8%; Score 1385.5; DB 10; Length 297;
Best Local Similarity 87.2%; Pred. No. 7.4e-136; Indels 1; Gaps 1;
Matches 260; Conservative 21; Mismatches 16;

```
Qy 1 MTEOAISFAKDFLAGGIAAISKTAVAPIERVKLLQVHASKQJIAADKQYKGIIDCVVR 60
Db 1 MGDHMSFLKDFLAGGVAALAAVSKTAVAPIERVKLLQVHASKQJIAEKQYKGIIDCVVR 60
Qy 61 IPKEGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDNKHQFMRFAGNLSAG 120
Db 61 IPKEGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDNKHQFMRFAGNLSAG 120
Qy 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREPFGDCLVKTIKSGICGLYOGFSVS 180
Db 121 GAAGATSLCFYVPLDFARTRLAADVGR-AGREFHGLDCLIKIKSGICGLYOGFSVS 179
Qy 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTIIVSWMIAQTVTAAGVSVSPEDTVRRMM 240
Db 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTIIVSWMIAQTVTAAGVSVSPEDTVRRMM 239
Qy 241 QSGRKGADIMYGTVDCKRKIFRDEGKAFKFGANSNVLRCMGAFVLVYDELK 298
Db 241 QSGRKGADIMYGTVDCKRKIFRDEGKAFKFGANSNVLRCMGAFVLVYDELK 297
```

RESULT 7
US-09-801-368-252
; Sequence 252, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Millne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801.368
; CURRENT FILING DATE: 2001-03-07

```

:
: PRIOR APPLICATION NUMBER: US 09/487,558
: PRIOR FILING DATE: 2000-01-19
: PRIOR APPLICATION NUMBER: US 60/160,587
: PRIOR FILING DATE: 1999-10-20
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: PatentIn Version 3.0
: SEQ ID NO 252
:
: LENGTH: 318
:
: TYPE: PR1
:
: ORGANISM: Saccharomyces cerevisiae
:
: US-09-801-368-252

```

Query Match:	49.3%	Score 760.5;	DB 10;	Length 318;
Best Local Similarity:	53.7%	Pred. No. 3,8e+71;		
Matches 159;	Conservative 42;	Mismatches 86;	Indels 9;	Gaps 5

[illegible]

```

RESULT 8
US-09-734-569-170
; Sequence 170, Application US/09734569
; Patent No. US20020064816A1
; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
; APPLICANT: Benz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reindl, Andreas
; APPLICANT: Clirpus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette
; APPLICANT: Duwenig, Elke
; APPLICANT: Schmidt, Ralf-Michael
; APPLICANT: Reski, Ralf
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
; TITLE OF INVENTION: in the synthesis of carbohydrates
; FILE REFERENCE: BASF-NbE-1332-99-US
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/171,101
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.1/Mordperfect 6.1
; SEQ ID NO 170
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-734-569-170

```

Query Match	48.68;	Score 749.5;	DB 10;	Length 386;
Best Local Similarity	53.48;	Pred. No. 6.7e-70;		
Matches 157;	Conservative 44;	Mismatches 84;	Indels 9;	Gaps 5;

Db	84	SPMTDFLNGVSAVSAKTAAPIERVKLLIIONDEMEKSGRLSPHYKIGGCSRTFYKDE	143
Qy	66	GVLSTWRGNLANVRIPEPTOLNFAFDKYOIFLGVDKHTQWRREFAGNILASGGAGA	125
Db	144	GMSLMSKRNITNVAITPEFTQOLNFAEKDYFSLSTGYKKD-DGYKKFAGNLASGGAGA	202
Qy	126	TSLSCHVPLDFAFTRLADV---GKSGTEREFKRLGDCLVKTKSDGIRGLYQGFYSVQ	182
Db	203	SLLFVYSLDVAKRLANDAKSSKKGGEERQFNGLVYKTKTALDTSIAGLYKRFALISCA	262
Qy	183	GIITIRRAYFECVYPTAK-MLPDKRNTHIVYSMMIAQTVAVNAGVSVPEPTVARRRMMQ	241
Db	263	GIYVRGLYEGYDLSKRVVLVGNLEGNFLASFLILGWITFGALASAPYDITVARRMMPT	322
Qy	242	SGRKADIMNYGTCVDCMKIRIDSGKRFPGGAMSNVLRGSGAFVVLVLEIK	295
Db	323	SGEA---VKYGSMDAFKQILLAKEANSLEFGAGANTIRAVAGCVLSTGDQLO	373

```

US-09-925-301-1459
; Sequence 1459, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatencIn Ver. 2.0
; SEQ ID NO 1459
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (126)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (129)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1459

```

Query Match	33.6%	Score 518	DB 10	Length 132
Best Local Similarity	96.3%	Pred. 1.4e-46		
Matches 103	Conservative	0	Mismatches 4	Indels 0
QY	1 MTEQATSPAKDFLAGGIAAISKTAAPAPLERKLLQYOVHASKQIADNRKYGIYDCIVR	60		
DB	26 MTEQATSPAKDFLAGGIAAISKTAAPAPLERKLLQYOVHASKQIADNRKYGIYDCIVR	85		
QY	61 IPRKQGVLSFWRGKGNLANVIRYPTQALNTAFKDKYKQIFLGGGDKHT	107		
DB	86 IPRKQGVLSFWRGKGNLANVIRYPTQALNTAFKDKYKQIFLGGGDKHT	132		

RESULT 10
US-09-864-761-36440
; Sequence 36440, Application US/0986476
; Patent No. US20020048763A1
; GENERAL INFORMATION:

[illegible]

APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tunas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic

```

RESULT 13
US-09-777-921A-5
: Sequence 5, Application US/09777921A
: Patent No. US20020115136A1
: GENERAL INFORMATION:
: APPLICANT: MERKULOV et al.
: TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CLO01103
: CURRENT APPLICATION NUMBER: US/09/777,921A
: CURRENT FILING DATE: 2002-02-07
: NUMBER OF SEQ ID NOS: 126
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 410
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-777-921A-5

```

1 CURRENT APPLICATION NUMBER: US/09/992,598
2
3 CURRENT FILING DATE: 2001-11-14
4
5 PRIOR APPLICATION NUMBER: 60/049787
6
7 PRIOR FILING DATE: 1997-06-16
8
9 PRIOR APPLICATION NUMBER: 60/062250
10
11 PRIOR FILING DATE: 1997-10-17
12
13 PRIOR APPLICATION NUMBER: 60/065186
14
15 PRIOR FILING DATE: 1997-11-12
16
17 PRIOR APPLICATION NUMBER: 60/065311
18
19 PRIOR FILING DATE: 1997-11-13
20
21 PRIOR APPLICATION NUMBER: 60/066770
22
23 PRIOR FILING DATE: 1997-11-24
24
25 PRIOR APPLICATION NUMBER: 60/075945
26
27 PRIOR FILING DATE: 1998-02-25
28
29 PRIOR APPLICATION NUMBER: 60/078910
30
31 PRIOR FILING DATE: 1998-03-20
32
33 PRIOR APPLICATION NUMBER: 60/083322
34
35 PRIOR FILING DATE: 1998-04-28
36
37 PRIOR APPLICATION NUMBER: 60/084600

[illegible]

1	PRIOR APPLICATION NUMBER: 60/087106
2	PRIOR FILING DATE: 1998-05-28
3	PRIOR APPLICATION NUMBER: 60/087607
4	PRIOR FILING DATE: 1998-06-02
5	PRIOR APPLICATION NUMBER: 60/087609
6	PRIOR FILING DATE: 1998-06-02
7	PRIOR APPLICATION NUMBER: 60/087759
8	PRIOR FILING DATE: 1998-06-02
9	PRIOR APPLICATION NUMBER: 60/087827
10	PRIOR FILING DATE: 1998-06-03
11	PRIOR APPLICATION NUMBER: 60/088021
12	PRIOR FILING DATE: 1998-06-04
13	PRIOR APPLICATION NUMBER: 60/088025
14	PRIOR FILING DATE: 1998-06-04
15	PRIOR APPLICATION NUMBER: 60/088026
16	PRIOR FILING DATE: 1998-06-04
17	PRIOR APPLICATION NUMBER: 60/088028
18	PRIOR FILING DATE: 1998-06-04
19	PRIOR APPLICATION NUMBER: 60/088029

RESULT 14
US-09-992-598-289
Sequence 289, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

RESULT 15
US-09-989-722-289
Sequence 289, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerilsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
PRIOR APPLICATION NUMBER: 2001-11-19
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349

```

: PRIOR FILING DATE: 1998-06-23
: PRIOR APPLICATION NUMBER: 60/090355
: PRIOR FILING DATE: 1998-06-23
: PRIOR APPLICATION NUMBER: 60/090429
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090431
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090435
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090444
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090445
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090472
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090535
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090540
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090542
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090557
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090676
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090678
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090690
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090694
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090695
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090696
: PRIOR FILING DATE: 1998-06-25
: PRIOR APPLICATION NUMBER: 60/090862
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: 60/090863
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: 60/091360
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091478
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091544
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091519
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091626
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091633
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091978
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/091982
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/092182
: PRIOR FILING DATE: 1998-07-09

```

```

Query Match      20.3%; Score 314; DB 10; Length 469;
Best Local Similarity 30.1%; Pred. No. 9.9e-25;
Matches 89; Conservative 60; Mismatches 115; Indels 32; Gaps 11;

```

```

Qy 10 KDFLAGGTAATSKTAVAPIERVKLLLOVHASKQIADKQKIVDCIVRIRPKQGVLS 69
Db 188 RHLVAVGGGAVSKTCTAFLDLRLKVLMOV-HASR-----SNMGIVGGFTOMIREGARS 241
Qy 70 FWRGNLAVIRYFTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLAAGAGATSLC 129
Db 242 LMRGNGINVLKTAPESAIKFMAIEQIKR--LVGSDQET---LRHRLVAGSLAGAIAS 296
Qy 130 FVYPLDFAFTRIALADVSGSTERFERGLDCLVKTITKSDGIRGLYOGFSVSVOGIITYRA 189
Db 297 SIYPMIEVLKTRMA--LRKTG---QYSGMLDCARILLAREGVAAFYKGYVFNNMGIITPYAG 351

```

```

Qy 190 AVEGYVDYAKGM-----LPDPKNTHLVYSWMIAGVTAYAG--VVSYPDFVRRMM 240
Db 352 IDLAYETLKNAWLOHYAVNSADPG----VFVLLACGTWSSTCGQLASTPLALVTRRQA 407
Qy 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFFKGANSVNLRGMGAFV--LVLYDELK 295
Db 408 QASIEGAPEVIMSSL--FKHLIRTEGAFGLYRGLAPNFPKVIIPAVISIVYVENLK 461

```

```

Search completed: November 12, 2002, 16:56:57
Job time : 7.34043 secs

```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:05 ; Search time 14.0157 Seconds
(without alignments)
2044.001 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MTEQALISFAADFLAGGIAA.....LRGNGAFVLYVDELKKVI 298

Scoring table:
BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1 S03894	ADP,ATP carrier pr
2	1512	98.0	298	2 B43646	ADP,ATP carrier pr
3	1454	94.2	298	1 A29132	ADP,ATP carrier pr
4	1424	92.3	298	1 I60173	adenine nucleotide
5	1422	92.2	298	1 XMBO	ADP,ATP carrier pr
6	1418	91.9	298	2 S37210	ADP,ATP carrier pr
7	1409	91.3	298	1 A44778	ADP,ATP carrier pr
8	1405	91.1	298	2 S31814	ADP,ATP carrier pr
9	1384	76.7	301	1 S31935	ADP,ATP carrier pr
10	1041	67.5	313	1 T23207	hypothetical prote
11	1039	67.3	313	2 T25850	hypothetical prote
12	1038	67.3	300	2 T25371	hypothetical prote
13	993.5	64.4	300	2 T15206	hypothetical prote
14	978	63.4	339	2 A41677	ADP,ATP carrier pr
15	943	61.1	301	2 S51132	ADP,ATP carrier pr
16	778.5	50.5	307	2 A36582	ADP,ATP carrier pr
17	772	50.0	308	1 S30259	ADP,ATP carrier pr
18	769	49.8	322	2 T40526	edp/atp translocas
19	768	49.8	386	2 T09709	ADP,ATP carrier pr
20	766	49.6	313	1 XMNC	ADP,ATP carrier pr
21	764	49.5	326	2 T25728	hypothetical prote
22	762.5	49.4	305	2 S68154	ADP,ATP carrier pr
23	760.5	49.3	318	1 A31978	ADP,ATP carrier pr
24	756.5	49.0	306	2 T30012	hypothetical prote
25	750	48.6	387	2 S14876	ADP,ATP carrier pr
26	748	48.5	386	2 S21974	ADP,ATP carrier pr
27	747	48.4	306	2 T42011	ADP,ATP carrier pr
28	747	48.4	386	2 S17917	ADP,ATP carrier pr
29	744	48.2	387	2 S16568	ADP,ATP carrier pr

30	743	48.2	379	2 T04608	ADP,ATP carrier pr
31	742.5	48.1	385	1 S29852	ADP,ATP carrier pr
32	742	48.1	382	2 S33630	ADP,ATP carrier pr
33	739.5	47.9	386	2 S14874	ADP,ATP carrier pr
34	737.5	47.8	309	2 A24849	ADP,ATP carrier pr
35	734.5	47.6	379	2 S21313	ADP,ATP carrier pr
36	681.5	44.2	298	2 T24029	hypothetical prote
37	520.5	33.7	327	2 T51577	ADP,ATP translocas
38	383	24.8	325	2 T04273	hypothetical prote
39	381	24.7	352	2 T01729	hypothetical prote
40	372	24.1	358	2 T45934	hypothetical prote
41	370.5	24.0	415	2 T48171	hypothetical prote
42	369.5	23.9	381	2 T51158	hypothetical prote
43	368	23.8	475	2 T50686	peroxisomal Ca-dep
44	363	23.5	348	2 D84798	probable mitochond
45	344.5	22.3	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1

S03894

ADP,ATP carrier protein T3 - human

N:Alternate names: ADP,ATP carrier protein T2 (misidentification): mitochondrial ADP,
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: S03894; B28116

R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:89236396; PMID:2541251
A:Accession: S03894

A:Status: not compared with conceptual translation
A:Molecule type: DNA

A:Residues: 1-298 <COG>
R:Howdsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: B28116
A:Molecule type: mRNA

A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
A:Cross-references: GB:J03392; NID:9339722; PIDN:AAA36750.1; PID:9339723

A:Experimental source: Liver
A:Genetics:

A:Gene: GDB:ANT3; ANT3Y
A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000

A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A>Note: There may be some confusion in the assignment of sequences for GDB:ANT2 and G
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP,ATP carrier protein repeat homology <ANT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1543; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 6.6e-129;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTEQALISFAKDFLAGGIAAISKTVAPTEERKLLQVQHASQIADKQRYGIVDCIYR	60
DB	1	MTEQALISFAKDFLAGGIAAISKTVAPTEERKLLQVQHASQIADKQRYGIVDCIYR	60
QY	61	IRKEGVLSFMRGNLANVIRYPTQALNFAFDKXKQIFLGGVDKHTQFWRFAAGNLASG	120
DB	61	IRKEGVLSFMRGNLANVIRYPTQALNFAFDKXKQIFLGGVDKHTQFWRFAAGNLASG	120
QY	121	GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGDLGCLVITKSDGIRGLYOGFSVS	180
DB	121	GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGDLGCLVITKSDGIRGLYOGFSVS	180

QY 181 VGGIIIRAAVFGVYDPAKMLDPKNTHTVSMIAQTAVAGVSYPPDVTYRRMM 240
 |||||
 Db 181 VGGIIIRAAVFGVYDPAKMLDPKNTHTVSMIAQTAVAGVSYPPDVTYRRMM 240

QY 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGKMSNVLRGMGAFVLYLDELKVI 298
 |||||
 Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGKMSNVLRGMGAFVLYLDELKVI 298

RESULT 2

B43646
 A:ADP/ATP carrier protein T2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: B43646
 A:Molecule type: mRNA
 A>Status: preliminary
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:g529416; PIDN:AAA30769.1; PID:g529417
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPi>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 98.0%; Score 1512; DB 2; Length 298;
 Best Local Similarity 97.7%; Pred. No. 3.6e-126;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEBAISFANDFLAGIAAIAISKTAVAPIERVKLLQVHASKOIAADKQKGIIDCVR 60
 |||||
 Db 1 MTEBAISFANDFLAGIAAIAISKTAVAPIERVKLLQVHASKOIAADKQKGIIDCVR 60

QY 61 IPKEGVLSPWGRNLAVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRFGNLSG 120
 |||||
 Db 61 IPKEGVLSPWGRNLAVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRFGNLSG 120

QY 121 GAAGATSLCFVYPLDFKARTRLADVCKSGSERFRGIGDCLVTKTSGDGRGLYOGFNS 180
 |||||
 Db 121 GAAGATSLCFVYPLDFKARTRLADVCKSGSERFRGIGDCLVTKTSGDGRGLYOGFNS 180

QY 181 VGGIIIRAAVFGVYDPAKMLDPKNTHTVSMIAQTAVAGVSYPPDVTYRRMM 240
 |||||
 Db 181 VGGIIIRAAVFGVYDPAKMLDPKNTHTVSMIAQTAVAGVSYPPDVTYRRMM 240

QY 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGKMSNVLRGMGAFVLYLDELKVI 298
 |||||
 Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGKMSNVLRGMGAFVLYLDELKVI 298

RESULT 3

A29132
 A:ADP/ATP carrier protein T2 - human
 N:Alternate names: mitochondrial ADP/ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132; C28116
 R:Ballini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262, 4355-4359, 1987
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat
 A:Reference number: A29132; MUID:87160056; PMID:3031073
 A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>
 A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R:Shouldsworth, J.; Altardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in

A:Reference number: A94197; MUID:88124845; PMID:2829183
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
 A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A:Experimental source: clone pHA73
 C:Genetics:
 A:Gene: GDB:ANT2; T3; 2F1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-Xq26
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G

C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPi>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 4.9e-121;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEBAISFANDFLAGIAAIAISKTAVAPIERVKLLQVHASKOIAADKQKGIIDCVR 60
 |||||
 Db 1 MTEBAISFANDFLAGIAAIAISKTAVAPIERVKLLQVHASKOIAADKQKGIIDCVR 60

QY 61 IPKEGVLSPWGRNLAVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRFGNLSG 120
 |||||
 Db 61 IPKEGVLSPWGRNLAVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRFGNLSG 120

QY 121 GAAGATSLCFVYPLDFKARTRLADVCKSGSERFRGIGDCLVTKTSGDGRGLYOGFNS 180
 |||||
 Db 121 GAAGATSLCFVYPLDFKARTRLADVCKSGSERFRGIGDCLVTKTSGDGRGLYOGFNS 180

QY 181 VGGIIIRAAVFGVYDPAKMLDPKNTHTVSMIAQTAVAGVSYPPDVTYRRMM 240
 |||||
 Db 181 VGGIIIRAAVFGVYDPAKMLDPKNTHTVSMIAQTAVAGVSYPPDVTYRRMM 240

QY 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGKMSNVLRGMGAFVLYLDELK 296
 |||||
 Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGKMSNVLRGMGAFVLYLDELK 296

RESULT 4

I60173
 A:adenine nucleotide translocator - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: I60173
 R:Shimohara, Y.; Kamida, M.; Yamazaki, N.; Teraida, H.
 Biochim. Biophys. Acta 1152, 192-196, 1993
 A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding r
 A:Reference number: I60173; MUID:94002161; PMID:8399300
 A:Accession: I60173
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-298 <RES>
 A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
 C:Genetics:
 A:Gene: ant1
 A:Introns: 37/3; 200/1; 247/1
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPi>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 92.3%; Score 1424; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 2.2e-118;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEBAISFANDFLAGIAAIAISKTAVAPIERVKLLQVHASKOIAADKQKGIIDCVR 60
 |||||
 Db 1 MTEBAISFANDFLAGIAAIAISKTAVAPIERVKLLQVHASKOIAADKQKGIIDCVR 60

QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRFAGNLNSG 120
|||||
Db 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRFAGNLNSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYVGKSGTEREFGDCLVKIRKSDIRGLYOGFSYS 180
|||||
Db 121 GAAGATSLCFVYPLDFARTRLADYVGKSGTEREFGDCLVKIRKSDIRGLYOGFSYS 180
QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVAAGVSPFDTVRRMM 240
|||||
Db 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVAAGVSPFDTVRRMM 240
QY 241 OSGRKGADIMYGTVDCKMRKIRFDEGKAFFGKAMSNVLRGGAFAVLVYDELKKVI 298
|||||
Db 241 OSGRKGADIMYGTVDCKMRKIRFDEGKAFFGKAMSNVLRGGAFAVLVYDELKKVI 298

RESULT 5

XMBO
ADP,ATP carrier protein T1 - bovine
N:Alternate names: ADP/ATP translocase T1
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
R:Accession: A43646; A24822; A03181; A61343; S69369
R:Powell, S.J.; Mead, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A>Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A:Reference number: A43646; MUID:89229093; PMID:2540808
A:Accession: A43646
A:Molecule type: mRNA
A:Residues: 1-298 <POM>
A:Cross-references: GB:M4102; NID:9529414; PIDN:AAA30768.1; PID:9529415
R:Rasmussen, U.B.; Wohlitz, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A>Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
A:Reference number: A24822; MUID:86295775; PMID:3017341
A:Accession: A24822
A:Molecule type: mRNA
A:Residues: 208-298 <RAS>
A:Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631
R:Aquila, H.; Mistr, D.; Eulitz, M.; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A>Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
A:Reference number: A03181; MUID:82188267; PMID:7076130
A:Accession: A03181
A:Molecule type: Protein
A:Residues: 2-51, 'X', '53-70, 'X', '72-109, 'X', '111-298 <AOU>
A>Note: residue 52 may be methyllysine
R:Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A>Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria
A:Reference number: A61343; MUID:82046808; PMID:6271240
A:Accession: A61343
A:Molecule type: protein
A:Residues: 205-298 <BAB>
R:Oettermeyer, W.; Masson, K.; Kalina, S.
Eur. J. Biochem. 227, 730-733, 1995
A>Title: [(3)H]-2-ido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
A:Reference number: S69369; MUID:95172058; PMID:7867632
A:Accession: S69369
A:Molecule type: protein
A:Residues: 49-63,154-168 <OET>
C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
C:Complex: homodimer
C:Function:
A:Note: located in the inner mitochondrial membrane
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

F:2/Modified site: acetylated amino end (Ser) (1n mature form) #status experimental
F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 92.2%; Score 1422; DB 1; Length 298;
Best Local Similarity 89.3%; Pred. No. 3.3e-118;
Matches 266; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGIAAISKTAVERKLLQVHASKQIAADKQYGYDCTYR 60
|||
Db 1 MDOALSFLLKDFLAGIAAISKTAVERKLLQVHASKQIAADKQYGYDCTYR 60
QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRFAGNLNSG 120
|||||
Db 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRFAGNLNSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYVGKSGTEREFGDCLVKIRKSDIRGLYOGFSYS 180
|||||
Db 121 GAAGATSLCFVYPLDFARTRLADYVGKSGTEREFGDCLVKIRKSDIRGLYOGFSYS 180
QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVAAGVSPFDTVRRMM 240
|||||
Db 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVAAGVSPFDTVRRMM 240
QY 241 OSGRKGADIMYGTVDCKMRKIRFDEGKAFFGKAMSNVLRGGAFAVLVYDELKKVI 298
|||||
Db 241 OSGRKGADIMYGTVDCKMRKIRFDEGKAFFGKAMSNVLRGGAFAVLVYDELKKVI 298

RESULT 6

S37210
ADP,ATP carrier protein T1 - mouse
N:Alternate names: adenine nucleotide carrier
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
R:Accession: S37210
R:Laplace, C.; Costet, P.
submitted to the EMBL Data Library, September 1993
A:Reference number: S37210
A:Accession: S37210
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <LAP>
A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628
C:Genetics: ANCI
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 91.9%; Score 1418; DB 2; Length 298;
Best Local Similarity 88.9%; Pred. No. 7.6e-116;
Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGIAAISKTAVERKLLQVHASKQIAADKQYGYDCTYR 60
|||
Db 1 MDOALSFLLKDFLAGIAAISKTAVERKLLQVHASKQIAADKQYGYDCTYR 60
QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRFAGNLNSG 120
|||||
Db 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRFAGNLNSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYVGKSGTEREFGDCLVKIRKSDIRGLYOGFSYS 180
|||||
Db 121 GAAGATSLCFVYPLDFARTRLADYVGKSGTEREFGDCLVKIRKSDIRGLYOGFSYS 180
QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVAAGVSPFDTVRRMM 240
|||||
Db 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVAAGVSPFDTVRRMM 240
QY 241 OSGRKGADIMYGTVDCKMRKIRFDEGKAFFGKAMSNVLRGGAFAVLVYDELKKVI 298
|||||
Db 241 OSGRKGADIMYGTVDCKMRKIRFDEGKAFFGKAMSNVLRGGAFAVLVYDELKKVI 298

QY 8 FAKPFLAGIAAISKTAAPVAPIERVKLLQVHASKQIAADKQYKIVDCIARIPEKQGV 67
 Db 12 FLIDLASGCTAAASVKTAAVPIERVKLLQVODASKAIAVDKRYKIMDVLIIRPKKQGV 71
 QY 68 LSPFRGNLANVIRYEPQALNFAFKDKYKQIFLGVDKHKHOFMKYFAGCNLASGGAAGATS 127
 Db 72 AALMRGNLANVIRYEPQALNFAFKDKYKQIFLEGDLKKDKFMKFFAGCNLASGGAAGATS 131
 QY 128 LCFVYPLDFAFTRTLAAVNGKSGTEREFGGLDCLVKTITKSDIGLVOGFVSVOGIITIIY 187
 Db 132 LCFVYPLDFAFTRTLAAVNGKSGTEREFGGLDCLVKTITKSDIGLVOGFVSVOGIITIIY 190
 QY 188 RAATFGYIDTAKGML-PDPKNTNHIYVSMIAQVTVAVAGVSYEPDVRRRMMQSGRGK 246
 Db 191 RAATFGYIDTAKGML-PDPKNTNHIYVSMIAQVTVAVAGVSYEPDVRRRMMQSGRGK - 249
 QY 247 ADIYTCGVDCWRKIFRDEGKAFKFGAMSIVLRMGAGAPVLYLYDELKKVI 298
 Db 250 -DILYKNTLDCARKIIONEGMSAMFKGALSIVFRGTGALVLAIDEIQFL 300

RESULT 13

T15206

hypothetical protein W02D3.6 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000

C/Accession: T15206

R/ile, T.; Weinstein, L.; Rifkin, L.

submitted to the EMBL data library, May 1997

A/Description: The sequence of C. elegans cosmid W02D3.

A/Reference number: Z18508

A/Accession: T15206

A/Status: preliminary; translated from GB/EMBL/DD83

A/Molecule type: DNA

A/Cross-references: EMBL:AF003141; NID:g2088732; PID:g2088738; PIDN:AAB54179.1; GSPDB:GN

A/Experimental source: Strain Bristol N2; clone W02D3

C/Genetics:

A/Gene: CESP:W02D3.6

A/Map position: 1

C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

F;9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>

Query Match

Best local Similarity 64.4%; Score 993.5; DB 2; Length 300;
 Matches 195; Conservative 40; Mismatches 59; Indels 7; Gaps 4;

QY 2 TEOAISRAK--DFLAGIAAISKTAAPVAPIERVKLLQVHASKQIAADKQYKIVDCI 58
 Db 3 TKEGFEDYRKELVDLASGTAIAISKTAAPVAPIERVKLLQVSDVSETVTADKKYKIMDVLI 62
 QY 59 VRIKEGVLSFMRGNLANVIRYEPQALNFAFKDKYKQIFLGVDKHKHOFMKYFAGCNLA 118
 Db 63 ARVKEGVLSFMRGNLANVIRYEPQALNFAFKDKYKQIFLGVDKHKHOFMKYFAGCNLA 122
 QY 119 SGGAAGATSLCFVYPLDFAFTRTLAAVNGKSGTEREFGGLDCLVKTITKSDIGLVOGFS 178
 Db 123 SGGAAGATSLCFVYPLDFAFTRTLAAVNGKSGTEREFGGLDCLVKTITKSDIGLVOGFS 181
 QY 179 VSVGGIITIRAAVFGVYDFAKGM-L-PDPKNTNHIYVSMIAQVTVAVAGVSYEPDVRRR 237
 Db 182 VSVGGIITIRAAVFGVYDFAKGM-L-PDPKNTNHIYVSMIAQVTVAVAGVSYEPDVRRR 241
 QY 238 MMQSGRGKADIMYTGVDCKRIFRDEGKAFKFGAMSIVLRMGAGAPVLYLYDELKKVI 297
 Db 242 MMQSGRGK--DILYKNTLDCARKIIONEGMSAMFKGALSIVFRGTGALVLAIDEIQHL 299
 QY 298 I 298
 Db 300 I 300

RESULT 14

A41677
 ADP,ATP carrier protein - Chlorella kessleri
 C/Species: Chlorella kessleri
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
 C/Accession: A41677
 R/Hilgath, C.; Sauer, N.; Tanner, W.
 J. Biol. Chem. 266, 24044-24047, 1991
 A/Title: Glucose increases the expression of the ATP/ADP translocator and the glycera
 A/Reference number: A41677; MUID:92084708; PMID:1748677
 A/Accession: A41677
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-339 <H>
 A/Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
 C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F;38-134/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F;112-235/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F;241-329/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match

Best local Similarity 66.9%; Score 978; DB 2; Length 339;
 Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

QY 6 ISFAKDEFLAGIAAISKTAAPVAPIERVKLLQVHASKQIAADK--QYKIVDCIARIPEK 63
 Db 39 MAFYKDLLAGTGTAGAIKSTAVAPIERVKLLQVSDVSETVTADKKYKIMDVLIIRPKKQGV 98
 QY 64 EQGVLFWNRGNLANVIRYEPQALNFAFKDKYKQIFLGVDKHKHOFMKYFAGCNLASGAA 123
 Db 99 EQGVLFWNRGNLANVIRYEPQALNFAFKDKYKQIFLGVDKHKHOFMKYFAGCNLASGAA 157
 QY 124 GATSLCFVYPLDFAFTRTLAAVNGKSGTEREFGGLDCLVKTITKSDIGLVOGFSVVOG 183
 Db 158 GAGSLVLYPLDFAFTRTLAAVNGKSGTEREFGGLDCLVKTITKSDIGLVOGFSVVOG 216
 QY 184 IIRYRAVFGVYDFAKGM-L-PDPKNTNHIYVSMIAQVTVAVAGVSYEPDVRRRMMQSG 242
 Db 217 IIRYRAVFGVYDFAKGM-L-PDPKNTNHIYVSMIAQVTVAVAGVSYEPDVRRRMMQSG 276
 QY 243 GRKADIMYTGVDCKRIFRDEGKAFKFGAMSIVLRMGAGAPVLYLYDELKKVI 298
 Db 277 --GGERQYNGTIDCWKRVAQDEGKAFKFGAMSIVLRMGAGAPVLYLYDELKKVI 329

RESULT 15

S51132

ADP,ATP carrier protein - malaria parasite (Plasmodium falciparum)

N/Alternate names: ADP/ATP transporter

C/Species: Plasmodium falciparum

C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000

C/Accession: S68993; S51132

R/Hall, T.; Jauregui, G.

A/Title: Molecular characterization of the ADP/ATP-transporter cDNA from the human ma

A/Reference number: S68993; MUID:95188918; PMID:7883016

A/Accession: S68993

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-301 <H>

A/Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335

C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C/Keywords: duplication; transmembrane protein

F;6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match

Best local Similarity 61.1%; Score 943; DB 2; Length 301;
 Matches 183; Conservative 45; Mismatches 62; Indels 6; Gaps 5;

QY 7 SFAPKDEFLAGIAAISKTAAPVAPIERVKLLQVHASKQIAAD--KQYKIVDCIARIPEK 64

Db 8 NEADFLMGISAIISKTVVPIERVKMLIQODSIPETIKSGOVERYSGLINCPRKVSKE 67
Qy 65 QCVLSFWNGNLNANVIRYFPTQALNFAFKDKYQOIFLGVDKHTOFWRFFAGNLASGGAAG 124
Db 68 QCVLSIMRGNNVNVIRYFPTQAFNFAFKDYFKNIF-PRYDQNTDFSKFECVNILSGATAG 126
Qy 125 ATSLEFVYPPLDFARTRLADVGKSGTEREPRGLGDCLVKITKSDGIRGLYOGFSVSGI 184
Db 127 AISLIVIPLDPARTRLASDICK-GKDRQFTGLFDCLAKIYKOTGLLSYSGFVSVYGI 185
Qy 185 IYRAAYFGVYDTAGML-PDPKNTIYVSMIAQVTAVAGVSYPEFTVRRMMMSG 243
Db 186 IYRGSYFGLYDSAKALLFTNDKNTNIVLKMAVAQSVTLAGLISYPEFTVRRMMMSG 245
Qy 244 RKG-ADIMYTGIVDCRKITFDEGKAFKFGAMSNVLRGMGAFVLYLYDELKVI 298
Db 246 RKGKEIQYKNTIDCMIKILRNEGFKFGKAMANYIRGAGALVLYFYDELQKLI 301

Search completed: November 12, 2002, 16:48:38
Job time : 15.0157 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:20 : Search time 7.67525 Seconds
(without alignments)
1610.364 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MTEQAISFAKDFLAGGIAA.....LRMGCAFVLYDELRKVI 298

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	ADP3_HUMAN	P12236 homo sapien
2	1512	98.0	298	ADP3_BOVIN	P32007 bos taurus
3	1463	94.8	298	ADP2_HUMAN	P05141 homo sapien
4	1451	94.0	298	ADP2_RAT	P09073 rattus norv
5	1445	93.6	298	ADP2_MOUSE	P51861 mus musculu
6	1428	92.3	298	ADP1_RAT	P05962 rattus norv
7	1418	91.9	298	ADP1_MOUSE	P48962 mus musculu
8	1417	91.8	297	ADP1_BOVIN	P02722 bos taurus
9	1409	91.3	298	ADP1_HUMAN	P12235 homo sapien
10	1217.5	78.9	297	ADP_ANCE	P26365 drosophila
11	1204	78.0	301	ADP_ANCE	P27238 anopheles g
12	978	63.4	339	ADP_CHLKE	P31692 chlorella k
13	778.5	50.5	307	ADP3_YEAST	P18238 saccharomyc
14	772	50.0	308	ADP_CHLRE	P27080 chlamydomon
15	769	49.8	322	ADP_SCHPO	P09188 schizosacch
16	768	49.8	386	ADP1_GOSHI	P02342 gossypium h
17	766	49.6	313	ADP_NEUCR	P02723 neurospora
18	762.5	49.4	305	ADP_KUDLA	P49382 kluyveromyc
19	760.5	49.3	318	ADP2_YEAST	P18238 saccharomyc
20	750.5	48.6	385	ADP2_ARATH	P40941 arabidopsis
21	750	48.6	387	ADP1_MAIZE	P04709 zea mays (m
22	748	48.5	386	ADP1_SOLTU	P25083 solanum tub
23	747	48.4	382	ADP_ORYSA	P31691 oryza sativ
24	744	48.2	387	ADP2_MAIZE	P12857 zea mays (m
25	742.5	48.1	381	ADP1_ARATH	P31167 arabidopsis
26	740	48.0	331	ADP1_WHEAT	P41629 triticum ae
27	739.5	47.9	386	ADP2_SOLTU	P27081 solanum tub
28	737.5	47.8	309	ADP1_YEAST	P04710 saccharomyc
29	727	47.1	331	ADP2_WHEAT	P41630 triticum ae
30	727	47.1	331	ADP2_WHEAT	P41630 triticum ae
31	300	19.6	588	GDC_BOVIN	P01888 bos taurus
32	299	19.4	307	ODC2_YEAST	P09297 saccharomyc
33	297	19.2	587	CMC3_CAEEL	Q19529 caenorhabdi

34	295	19.1	678	1	CMC1_HUMAN	O75746 homo sapien
35	289.5	18.8	322	1	GDC_RAT	P16261 rattus norv
36	287.5	18.6	702	1	CMC1_CAEEL	O21153 caenorhabdi
37	286	18.5	325	1	UCP5_HUMAN	O95258 homo sapien
38	285	18.5	332	1	GDC_HUMAN	P16260 homo sapien
39	284	18.4	325	1	UCP5_MOUSE	O94282 mus musculu
40	282.5	18.3	326	1	YE08_SCHPO	O13805 schizosacch
41	280	18.1	675	1	CMC2_HUMAN	O94930 homo sapien
42	272	17.6	315	1	MPT_HUMAN	O942d1 homo sapien
43	270	17.5	315	1	SA18_HUMAN	O941k4 homo sapien
44	265	17.2	312	1	UCP3_HUMAN	P55916 homo sapien
45	265	17.2	676	1	CMC2_MOUSE	O94xx4 mus musculu

ALIGNMENTS

```

RESULT 1
ADP3_HUMAN
ID ADP3_HUMAN STANDARD: PRT: 298 AA.
AC P12236; 096C49;
DT 01-OCT-1989 (Rel. 12, Created)
DR 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP, ATP carrier protein, liver isoform P2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RA Margolin J.F.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Cervix, Eye, and Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houdsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
RN [5]
RP FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
RP MITOCHONDRIAL INNER MEMBRANE.
RN [6]
RP SUBUNIT: HOMODIMER.
RN [7]
RP SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
RP inner membrane.
RN [8]
RP - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
RN [9]
RP - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
RN [10]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
RP between the Swiss Institute of Bioinformatics and the EMBL outstation -
RP the European Bioinformatics Institute. There are no restrictions on its
RP use by non-profit institutions as long as its content is in no way
RP modified and this statement is not removed. Usage by and for commercial
RP entities requires a license agreement (See http://www.isb-sib.ch/announce/
RP or send an email to license@sib-sib.ch).
RN [11]
RP EMBL: J03592; AAA36750.1;

```

DR EMBL: AY007135; AAC01998.1; -.
 DR EMBL: BC007295; AAH07295.1; -.
 DR EMBL: BC007850; AAH07850.1; -.
 DR EMBL: BC008373; AAH08373.1; -.
 DR EMBL: BC008935; AAH08935.1; -.
 DR EMBL: BC014775; AAH14775.1; -.
 DR PIR: S03894; S03894.
 DR PIR: B28116; B28116.
 DR Genew: HGNC:10992; SLC25A6.
 DR MIM: 300151; -.
 DR MIM: 403000; -.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 105 108 S -> F (IN REF. 3; AAH14775).
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
 SQ SEQUENCE 298 AA; 32866 MM; 18534E9F0E49672F CRC64;

Query Match 100.0%; Score 1543; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 5.3e-130;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLLOVHASKOIAADKQYKGIIVDCIVR 60
 DB 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLLOVHASKOIAADKQYKGIIVDCIVR 60
 QY 61 IPKQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSAG 120
 DB 61 IPKQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSAG 120
 QY 121 GAAGATSLCFEYYPIDFARTRLADVGKSGTEREFGDCLVTKTSKGIRGLYQGSFVS 180
 DB 121 GAAGATSLCFEYYPIDFARTRLADVGKSGTEREFGDCLVTKTSKGIRGLYQGSFVS 180
 QY 121 GAAGATSLCFEYYPIDFARTRLADVGKSGTEREFGDCLVTKTSKGIRGLYQGSFVS 180
 DB 121 GAAGATSLCFEYYPIDFARTRLADVGKSGTEREFGDCLVTKTSKGIRGLYQGSFVS 180
 QY 181 VQGITIRAAAFGYVDPAKGMLPDPKNTHTVSMIAQTAVAGVSYSPEDTVRRRRMM 240
 DB 181 VQGITIRAAAFGYVDPAKGMLPDPKNTHTVSMIAQTAVAGVSYSPEDTVRRRRMM 240
 QY 241 QSGRRGADIMYTGIVDCWRKIFRDEGKAFKFGAMSIVLRMGCAFVLYLYDELKKVI 298
 DB 241 QSGRRGADIMYTGIVDCWRKIFRDEGKAFKFGAMSIVLRMGCAFVLYLYDELKKVI 298

RESULT 2
 ADT3_BOVIN
 ID ADT3_BOVIN STANDARD; PRT; 298 AA.
 AC P32007;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP, ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (adenine nucleotide translocator 3) (ANT 3).
 GN SLC25A6 OR ANT3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovidae; Bos.
 OC NCBI_TaxID=9913;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE:89229093; PubMed-2540808;
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
 RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
 RT differences in various tissues.";
 RL Biochemistry 28:866-873(1989).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M24103; AAA30769.1; -.
 DR PIR: B43646; B43646.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32877 MM; 1C34E7DF6EDE4061 CRC64;

Query Match 98.0%; Score 1512; DB 1; Length 298;
 Best Local Similarity 97.7%; Pred. No. 3e-127;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLLOVHASKOIAADKQYKGIIVDCIVR 60
 DB 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLLOVHASKOIAADKQYKGIIVDCIVR 60
 QY 61 IPKQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSAG 120
 DB 61 IPKQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSAG 120
 QY 121 GAAGATSLCFEYYPIDFARTRLADVGKSGTEREFGDCLVTKTSKGIRGLYQGSFVS 180
 DB 121 GAAGATSLCFEYYPIDFARTRLADVGKSGTEREFGDCLVTKTSKGIRGLYQGSFVS 180
 QY 121 GAAGATSLCFEYYPIDFARTRLADVGKSGTEREFGDCLVTKTSKGIRGLYQGSFVS 180
 DB 121 GAAGATSLCFEYYPIDFARTRLADVGKSGTEREFGDCLVTKTSKGIRGLYQGSFVS 180
 QY 181 VQGITIRAAAFGYVDPAKGMLPDPKNTHTVSMIAQTAVAGVSYSPEDTVRRRRMM 240
 DB 181 VQGITIRAAAFGYVDPAKGMLPDPKNTHTVSMIAQTAVAGVSYSPEDTVRRRRMM 240
 QY 241 QSGRRGADIMYTGIVDCWRKIFRDEGKAFKFGAMSIVLRMGCAFVLYLYDELKKVI 298
 DB 241 QSGRRGADIMYTGIVDCWRKIFRDEGKAFKFGAMSIVLRMGCAFVLYLYDELKKVI 298

RESULT 3
 ADT2_HUMAN
 ID ADT2_HUMAN STANDARD; PRT; 298 AA.
 AC P05141; O43350.
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 GN (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=90375457; PubMed=2168878;
 RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Muzzel J.;
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular
 cloning and sequence.";
 RL J. Biol. Chem. 265:16060-16063(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87166056; PubMed=3031073;
 RA Battini R., Ferrarri S., Kaczmarek L., Calabretta B., Chen S.T.,
 RA Baserga R.;
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
 growth-regulated.";
 RL J. Biol. Chem. 262:4355-4358(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagataja R.,
 RA Mazzarella R.A., Schlessinger D., Chen E.Y.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Becker M., Graves T., Ozerky P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 47-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houdsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M57424; AA51737.1; -
 DR EMBL: J02683; AA35579.1; -
 DR EMBL: L78810; AA83926.1; -
 DR EMBL: AC004000; AA86347.1; -
 DR EMBL: J03591; AA36749.1; -
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR Genem; HGNC:10991; SLC25A5.
 DR MIM: 300150; -
 DR InterPro: IPR002067; MtcCarrier.
 DR InterPro: IPR001993; MitoChCarrier.
 DR Pfam: PF00153; MitoCarri_3.
 DR PRINTS: PR00926; MITOCHARRIER.
 DR PROSITE: PS00215; MITOCHARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 FT MultiGene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).

FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA: 32895 MW: F973C3AED92C49D3 CR664;
 Query Match 94.8%; Score 1463; DB 1; Length 298;
 Best Local Similarity 92.9%; Pred. No. 6; 9e-123;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MPEQATSEFAKDFLAGIAAISTAVPIERVKLLIQVHASKQIADKQYGVNDCYVR 60
 DB 1 MPEQATSEFAKDFLAGIAAISTAVPIERVKLLIQVHASKQIADKQYGVNDCYVR 60
 QY 61 IPEQGVLSFMRGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFMRFFAGNLAG 120
 DB 61 IPEQGVLSFMRGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFMRFFAGNLAG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGDGLVYTKSDGIRGLYGFVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGDGLVYTKSDGIRGLYGFVS 180
 QY 181 VGGIITTYRAAYRGVDTAGMLPDPKNTHTIYVSMIAQVTVAVAGVSPFDVRRRMM 240
 DB 181 VGGIITTYRAAYRGVDTAGMLPDPKNTHTIYVSMIAQVTVAVAGVSPFDVRRRMM 240
 QY 241 QSGRKADIMYGTVDCKRIFFDEGKAFKFGKMSNVLRGMGAFVLVYDELKK 296
 DB 241 QSGRKADIMYGTVDCKRIFFDEGKAFKFGKMSNVLRGMGAFVLVYDELKK 296
 RESULT 4
 ADP2_RAT STANDARD; PRT; 298 AA.
 ID ADP2_RAT
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D12771; BAA0238.1; -.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;
 Query Match 94.0%; Score 1451; DB 1; Length 298;
 Best Local Similarity 91.9%; Pred. No. 8e-122;
 Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQAISFAKDFLAGIAAISKTAVAPIERVKLLQVHASKIOIADKQYKGIIVDCIVR 60
 DB 1 MTDAAVSFADDFLAGVAAAIKSTAVAPIERVKLLQVHASKIOITADKQYKGIIDCVR 60
 QY 61 IPKEQGLSEWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFWRFFAGNLASG 120
 DB 61 IPKQGLSEWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFWRFFAGNLASG 120
 QY 121 GAAGATSLCFYYPPLDFARTRIADVKGSGTEREERGLGDCIVKTKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFYYPPLDFARTRIADVKGSGTEREERGLGDCIVKTKSDGIRGLYQGFVS 180
 QY 181 VQGIITRAAFYGYVDYDAKGMPLPPKNTHTVSMIAQTYAVAGVSYPPDYVRRRRMM 240
 DB 181 VQGIITRAAFYGYVDYDAKGMPLPPKNTHTVSMIAQTYAVAGVSYPPDYVRRRRMM 240
 QY 241 QSGRRGADIMYTGVDCKRKIFRDEGGAFFKGAAMSVNLRGMSGAFVLYLDELKK 296
 DB 241 QSGRRGADIMYTGVDCKRKIFRDEGGAFFKGAAMSVNLRGMSGAFVLYLDELKK 296
 RESULT 5
 ADT2_MOUSE STANDARD; PRT; 298 AA.
 ID ADT2_MOUSE
 AC P51881; 061311;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; Pubmed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 RT homologs.";
 RL Mamm. Genome 7:25-30(1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Sheldon J.G.;
 RL Thesis (1995), University of Cambridge, U.K.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA Costet P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP REVIEWS.
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20432087; Pubmed=10974536;
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 RT translocase 1 and 2 genes.";
 RL Gene 254:57-66(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U27316; AAC52838.1; -.
 DR EMBL: U10404; AAA19009.1; -.
 DR EMBL: X70847; CAA50196.1; -.
 DR EMBL: AF240003; AAF64471.1; -.
 DR MGI: MGI:1353496; SLC25a5.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;
 Query Match 93.6%; Score 1445; DB 1; Length 298;
 Best Local Similarity 91.6%; Pred. No. 2.7e-121;
 Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MTEQAISFAKDFLAGIAAISKTAVAPIERVKLLQVHASKIOIADKQYKGIIVDCIVR 60
 DB 1 MTDAAVSFADDFLAGVAAAIKSTAVAPIERVKLLQVHASKIOITADKQYKGIIDCVR 60
 QY 61 IPKEQGLSEWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFWRFFAGNLASG 120
 DB 61 IPKQGLSEWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFWRFFAGNLASG 120
 QY 121 GAAGATSLCFYYPPLDFARTRIADVKGSGTEREERGLGDCIVKTKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFYYPPLDFARTRIADVKGSGTEREERGLGDCIVKTKSDGIRGLYQGFVS 180

Db 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREPKGLDCLVYKISDGIKGLYGFNFS 180
Qy 181 VGGIIIRAAVFGVYDTAKGMLPDPKRNTHIVVSMIAQVTYAVAGVSYPFDTVRRMM 240
Db 181 VGGIIIRAAVFGVYDTAKGMLPDPKRNTHIVVSMIAQSVTAVAGVSYPFDTVRRMM 240
Qy 241 OSGRKGADIMYGTDCMKRIFRDEGKAFKFGAMSNVLRGAGAVLVLYDEIKV 296
Db 241 OSGRKGADIMYGTDCMKRIFRDEGKAFKFGAMSNVLRGAGAVLVLYDEIKV 296

RESULT 6
ADTL_RAT STANDARD: PRT: 298 AA.
ID ADTL_RAT
AC 005962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANTL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinozuka Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator.",
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER EXTENT, IN BRAIN AND KIDNEY.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X61667; CAA43842.1; -;
DR EMBL: D12770; BAA02237.1; -;
DR InterPro: IPR002067; MLC_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3;
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
KW TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA: 32969 MM: 66704FF78C6BC320 CRC64:

Query Match 92.3%; Score 1424; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 2e-119;

Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
Qy 1 MFEQATSEAKDPLAGIAAIAIKTAVAPIERVKLLIQVHASKQIAADKQYGIYDCIVR 60
Db 1 MCDQALSFKDKFLAGIAAASVSTAVAPIERVKLLIQVHASKQIAAEKQYGIIDCVVR 60
Qy 61 IRKEGVISFMWGNLANVIRYPTQALNFAFDKQYQIFLGVDKHTQWRFAAGLAAAG 120
Db 61 IRKEGVISFMWGNLANVIRYPTQALNFAFDKQYQIFLGVDKHTQWRFAAGLAAAG 120
Qy 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREPKGLDCLVYKISDGIKGLYGFNFS 180
Db 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREPKGLDCLVYKISDGIKGLYGFNFS 180
Qy 181 VGGIIIRAAVFGVYDTAKGMLPDPKRNTHIVVSMIAQVTYAVAGVSYPFDTVRRMM 240
Db 181 VGGIIIRAAVFGVYDTAKGMLPDPKRNTHIVVSMIAQSVTAVAGVSYPFDTVRRMM 240
Qy 241 OSGRKGADIMYGTDCMKRIFRDEGKAFKFGAMSNVLRGAGAVLVLYDEIKV 296
Db 241 OSGRKGADIMYGTDCMKRIFRDEGKAFKFGAMSNVLRGAGAVLVLYDEIKV 296

RESULT 7
ADTL_MOUSE STANDARD: PRT: 298 AA.
ID ADTL_MOUSE
AC P48962; 062164;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1) (MANT1).
GN SLC25A4 OR ANTL OR ANCL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse homologs.",
RL Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c; TISSUE=Muscle;
RA Laplace C., Costet P.;
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.",
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

DB 121 AAGATSLCEVYPLDFARTRRLADVGKGAQREFTGNGCITKIFKSDGLRGLYOGFNVS 180
 OY 182 OGIIIRAAVFGVYDTAGKMLPDPKNTIIVSMIAQVTAVAGVSYFPDTRRRMMQ 241
 DB 181 OGIIIRAAVFGVYDTAGKMLPDPKNTIIVSMIAQVTAVAGVSYFPDTRRRMMQ 240
 OY 242 SGRKADIMYCTVCCWKRIFRDEGKAFKFGKANSVLRGKMGATVLYYDELKVI 298
 DB 241 SGRKADIMYCTVCCWKRIFRDEGKAFKFGKANSVLRGKMGATVLYYDELKVI 297
 RESULT 9
 ADTL_HUMAN
 ID ADTL_HUMAN STANDARD: PRT: 298 AA.
 AC P12235;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89340499; PubMed=2547778;
 RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
 RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
 RT "A human muscle adenine nucleotide translocator gene has four exons,
 RT is located on chromosome 4, and is differentially expressed.";
 RL J. Biol. Chem. 264:13998-14004(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041149; PubMed=2823266;
 RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
 RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
 RT of a leader peptide, divergence from a fibroblast translocator cDNA,
 RT and coevolution with mitochondrial DNA genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-37 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 RN [6]
 RP VARIANTS PRO-114 AND MET-289.
 RX MEDLINE=20385067; PubMed=10926541;
 RA Kaukonen J., Juselius J.K., Tiranli V., Kyttala A., Zeviani M.,
 RA Komu G.P., Keranen J., Peltonen L., Suomalainen A.;
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
 RL Science 289:782-785(2000)
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
 CC progressive external ophthalmoplegia with various mitochondrial
 CC DNA deletions (PEO). Patients with PEO have mitochondrial
 CC myopathy, progressive external ophthalmoplegia, and other
 CC abnormalities associated with multiple different deletions of
 CC mitochondrial DNA.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: J02966; AAA61223.1; -;
 CC EMBL: J03593; AAA36751.1; -;
 CC EMBL: J04982; AAA51736.1; -;
 CC EMBL: BC008664; AAH08664.1; -;
 CC PIR: A28116; A28116.
 CC PIR: A39891; A39891.
 CC PIR: S03893; S03893.
 CC PIR: A44778; A44778.
 CC Genew: HGNC:10990; SLC25A4.
 CC MIM: 103220; -;
 CC MIM: 157640; -;
 CC InterPro: IPR002067; Mlt_carrier.
 CC InterPro: IPR001993; Mitoch_carrier.
 CC Pfam: PF00153; mito_carr. 3;
 CC PRINTS: PR00926; MITOCARRIER.
 CC PROSITE: PS00215; MITOCH_CARRIER. 3.
 CC KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 CC MultiGene family; Disease mutation.
 CC FT TRANSMEM 12 29 1 (POTENTIAL).
 CC FT TRANSMEM 73 91 2 (POTENTIAL).
 CC FT TRANSMEM 117 134 3 (POTENTIAL).
 CC FT TRANSMEM 176 195 4 (POTENTIAL).
 CC FT TRANSMEM 214 231 5 (POTENTIAL).
 CC FT TRANSMEM 273 291 6 (POTENTIAL).
 CC FT REPEAT 1 110 1.
 CC FT REPEAT 111 208 2.
 CC FT REPEAT 209 298 3.
 CC FT VARIANT 114 114 A -> P (IN PEO).
 CC FT VARIANT 289 289 /FTID-VAR_012111.
 CC FT VARIANT 289 289 V -> M (IN PEO).
 CC FT CONFLICT 16 16 G -> A (IN REF. 3).
 CC FT CONFLICT 147 149 KCA -> RR (IN REF. 3).
 CC FT CONFLICT 227 227 V -> L (IN REF. 3).
 CC FT CONFLICT 227 227 V -> L (IN REF. 3).
 CC SQ SEQUENCE 298 AA; 33064 MW; 59P0DFAEC4ETCFBB CRC64;
 Query Match 91.3%; Score 1409; DB 1; Length 298;
 Best Local Similarity 88.3%; Pred No. 4.4e-118;
 Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;
 OY 1 MTEQATSFADKPLAGGIAAISKTAVALPIERVKLLQVOHASQIADKQYGYDVCIVR 60
 DB 1 MGDHAWSLKDFLAGGVAANAASKTAVAPIERVKLLQVOHASQIADKQYGYDVCIVR 60
 OY 61 IRKEGCVLSFMKGNLANVIRFPYQALNFAFDKYKQIFLGVDKTKQYWRFPAGLASC 120
 DB 61 IRKEGCVLSFMKGNLANVIRFPYQALNFAFDKYKQIFLGVDKTKQYWRFPAGLASC 120
 OY 121 GAAGATSLCEVYPLDFARTRRLADVGKGAQREFTGNGCITKIFKSDGLRGLYOGFNVS 180
 DB 121 GAAGATSLCEVYPLDFARTRRLADVGKGAQREFTGNGCITKIFKSDGLRGLYOGFNVS 180
 OY 181 OGIIIRAAVFGVYDTAGKMLPDPKNTIIVSMIAQVTAVAGVSYFPDTRRRMMQ 240
 DB 181 OGIIIRAAVFGVYDTAGKMLPDPKNTIIVSMIAQVTAVAGVSYFPDTRRRMMQ 240
 OY 242 SGRKADIMYCTVCCWKRIFRDEGKAFKFGKANSVLRGKMGATVLYYDELKVI 298
 DB 242 SGRKADIMYCTVCCWKRIFRDEGKAFKFGKANSVLRGKMGATVLYYDELKVI 297

QY 241 OSGRKGADIMYGTGVCWKRIIFRDEGSKAFKFGAMSVNLGGMGAFLVLYDELKRYV 298
 DB 241 OSGRKGADIMYGTGVCWKRIIFRDEGSKAFKFGAMSVNLGGMGAFLVLYDELKRYV 298
 RESULT 10
 ADT_DROME STANDARD; PRT; 297 AA.
 AC Q26365; Q26254; P91614; O9V270;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT) (stress sensitive B protein).
 GN SCSB OR A/A-T OR CG16944.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92389367; PubMed=1387687;
 RA Louvi A., Tzitolou S.G.;
 RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila melanogaster shows a high degree of similarity with the mammalian ADP/ATP translocases.";
 RL J. Mol. Evol. 35:44-50(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94350065; PubMed=7520869;
 RA Hutter P., Karch F.;
 RT "Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila.";
 RL Experientia 50:749-762(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Oregon-R.
 RA Zhang Y.Q., Davis A.W., Roote J., Hermann S., Ashburner M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D., Wen R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolisakov S., Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson R., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris W., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin L., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D., Merkllov G., Milshina N.V., Mobarry C., Morris J., Moshirei A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H., Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,

RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; S43651; AAB23114.1; -;
 DR EMBL; S71762; AAB31734.3; -;
 DR EMBL; Y10618; CAA71628.1; -;
 DR EMBL; AE003484; AAF47957.1; -;
 DR FlyBase; FBgn0003360; seeb.
 DR InterPro; IPR002067; MLC_carrier.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carri; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 KW TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 177 196 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 272 290 6 (POTENTIAL).
 FT CONFLICT 18 19 QV -> GI (IN REF. 3 AND 4).
 FT CONFLICT 81 81 I -> Y (IN REF. 1).
 FT CONFLICT 200 200 R -> RG (IN REF. 3 AND 4).
 FT CONFLICT 266 266 G -> A (IN REF. 2).
 FT CONFLICT 267 268 PC -> TGA (IN REF. 3 AND 4).
 FT CONFLICT 268 268 C -> S (IN REF. 1).
 SQ SEQUENCE 297 AA; 32880 MW; AA639439968F9750 CRC64;
 Query Match 78.9%; Score 1217.5; DB 1; Length 297;
 Best local Similarity 79.3%; Pred. No. 4.7e-101;
 Matches 233; Conservative 24; Mismatches 34; Indels 3; Gaps 3;
 QY 5 AISAAPKFLAGGTAIAISKTAIVAPIERVKLLLOVQHASKQIADADKYKGYVDCIVRIPE 64
 DB 7 AVGVGFPAAGGOVSAASKTAIVAPIERVKLLLOVQHSKQISPDQKQYKGVWDFIRIPKE 66
 QY 65 QGVSEFWRGNLANTYRREPQALNFAFKDKYKQIFLGVDVKHGFQWFFYFPGNLASGGA 124
 DB 67 QGVSEFWRGNLANTYRREPQALNFAFKDKYKQIFLGVDVKHGFQWFFYFPGNLASGGA 126
 QY 125 ATSLCFYVPLDFAFTRIAADVGKSTREFRGLDCLVKTTSKSDIGLQGFSESVQGI 184
 DB 127 ATSLCFYVPLDFAFTRIAADVGKSG -QRETFGLGNCILTKIFKSDGIVGLRGFVSGGI 185
 QY 185 IITYAAVFGYDTAKGMLPDKKNTHTIVSWIAQTVTAAGVSVPPDYVRRRMMQSGR 244
 DB 186 IITYAAVFGYDTAKGMLPDKKNTHTIVSWIAQTVTAAGVSVPPDYVRRRMMQSGR 244
 QY 245 KGAIDIMYGTGVCWKRIIFRDEGSKAFKFGAMSVNLGGMGAFLVLYDELKRYV 298
 DB 245 KATEVITKNTLHCWATIAKQD -GPCFFKGAFSNLRKGTGGAFLVLYDELKRYV 297

RESULT 11

ADT_ANOGA STANDARD: PRT: 301 AA.

AC Q27238: 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).

OS Anopheles gambiae (African malaria mosquito).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

OX NCBI_TaxID=7163;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=G3;

RX MEDLINE=94348635; PubMed=8069414;

RA Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;

RT "A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.";

RL Insect Mol. Biol. 3:35-40(1994).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

CC EMBL: L11618; AAB04104.1; -

DR EMBL: L11617; AAB04105.1; -

DR InterPro: IPR002067; Mlt_carrier.

DR InterPro: IPR001993; Mitoch_carrier.

DR Pfam: PF00153; mito_carr: 3.

DR PRINTS: PR00926; MITOCARRIER.

DR PROSITE: PS00215; MITOCH_CARRIER: 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 14 31 1 (POTENTIAL).

FT TRANSMEM 75 93 2 (POTENTIAL).

FT TRANSMEM 119 136 3 (POTENTIAL).

FT TRANSMEM 178 197 4 (POTENTIAL).

FT TRANSMEM 216 233 5 (POTENTIAL).

FT TRANSMEM 275 293 6 (POTENTIAL).

SO SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;

Query Match 78.0%; Score 1204; DB 1; Length 301;

Best Local Similarity 77.7%; Pred. No. 7.5e-100;

Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

QY 1 MTEQA--ISFADFLAGTAAISTKTAVPRIERVKLLLOVQASHKQIADKQYKGI VDCI 58

DB 1 MTKKADPYGFAKDFLAGGISAASVSKTAVPRIERVKLLLOVQASHKQIADKQYKGI VDCI 60

QY 59 VAIPKEDGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIITLGVGVDKHTQEMRYEAGNLA 118

DB 61 VAIPKEDGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIITLGVGVDKHTQEMRYEAGNLA 120

QY 119 SGGAAGATSLCFVYPLDFARTRLADVGKSGTEREFGIGDCLVTKTSDDGIRGLYOGGS 178

DB 121 SGGAAGATSLCFVYPLDFARTRLADVGKSGTEREFGIGDCLVTKTSDDGIRGLYOGGS 180

QY 179 VSVGGIITIRAAVFGVYDTAKGMLDPPKNTHTVSWMIAQTVAVAGVVSYPFDVTRRM 238

DB 181 VSVGGIITIRAAVFGCFDTAKGMLDPPKNTHTVSWMIAQVTTASGIIYFPDVTYRRM 240

QY 239 NMOSGRKADIMYTGTVDCKMRIFRDEGGKAFKGAWSNVLRGMAFVLVYDELKVI 298

DB 241 NMOSWPKSEVMYKNTLDCWKVIGKQESGAFKGAWSNVLRGMAFVLVYDEVKALL 300

RESULT 12

ADT_CHLKE STANDARD: PRT: 339 AA.

AC P31692:

DT 01-JUL-1993 (Rel. 26, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).

OS Chlorella kessleri.

OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorella.

OX NCBI_TaxID=3074;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92084708; PubMed=1748677;

RA Hilgarch C., Sauer N., Tanner W.;

RT "Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";

RL J. Biol. Chem. 266:24044-24047(1991).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

CC EMBL: M76669; AAA33027.1; -

DR PIR: A41677; A41677.

DR InterPro: IPR002067; Mlt_carrier.

DR InterPro: IPR001993; Mitoch_carrier.

DR Pfam: PF00153; mito_carr: 3.

DR PRINTS: PR00926; MITOCARRIER.

DR PROSITE: PS00215; MITOCH_CARRIER: 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 45 62 1 (POTENTIAL).

FT TRANSMEM 108 126 2 (POTENTIAL).

FT TRANSMEM 151 168 3 (POTENTIAL).

FT TRANSMEM 209 228 4 (POTENTIAL).

FT TRANSMEM 248 265 5 (POTENTIAL).

FT TRANSMEM 304 322 6 (POTENTIAL).

SO SEQUENCE 339 AA; 36686 MW; 54779734A3B3942 CRC64;

Query Match 63.4%; Score 978; DB 1; Length 339;

Best Local Similarity 66.9%; Pred. No. 1.1e-79;

Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

QY 6 ISFADFLAGTAAISTKTAVPRIERVKLLLOVQASHKQIADK--QYKGI VDCI RPK 63

DB 39 MAFVKDLLAGTAAISTKTAVPRIERVKLLLOVQASHKQIADKQYKGI VDCI RPK 98

QY 64 ECGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIITLGVGVDKHTQEMRYEAGNLA 123

DB 99 ECGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIITLGVGVDKHTQEMRYEAGNLA 157

QY 124 GATSLCFVYPLDFARTRLADVGKSGTEREFGIGDCLVTKTSDDGIRGLYOGGS 183

```

Db 158 GAGSLIVPLDFAFRLADAVG--SGKSRFETGLVDCISKVRKRGGMALYQGFVSGVQG 216
QY 184 IITRYRAAYFVYDTAKGML-PDPKNTIIVYSMMIAQVTYAVGVSPPTVRRMMOS 242
Db 217 IITRYRAAYFVYDTAKGML-PDPKNTIIVYSMMIAQVTYAVGVSPPTVRRMMOS 276
QY 243 GRKADIMYGTVDWCKRIFRDEGKAFKFGKANSNVLKRGMGAFVLYDELKVI 298
Db 277 ---GGENVGTITDCWRKVAQOGKMAFFKGSNSNVLKRGMGAFVLYDELKVI 329

RESULT 13
ADT3_YEAST STANDARD: PRT: 307 AA.
AC P18238:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP/ATP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide
translocator 3) (ANT 3).
GN AAC3 OR YBR085W OR YBR0753.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE=90324259; PubMed=2165073;
RT Kolarova J., Kolarova N., Nelson N.;
RL "A third ADP/ATP translocator gene in yeast.";
RL J. Biol. Chem. 265:12711-12716(1990).
RN 12
RP SEQUENCE FROM N.A.
RA STRAIN=S288c;
RC STRAIN=S288c;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE OF 38-307 FROM N.A.
RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M34076; AAA97485.1; -
DR EMBL: Z35954; CAAB5031.1; -
DR PIR: A36582; A36582.
DR SGD: S0000289; AAC3.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mltch_carrier.
DR Pfam: PF00153; mltc_carri; 3.
DR PRINTS: PR00926; MITOCH_CARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 16 33 1 (POTENTIAL).
FT TRANSMEM 78 96 2 (POTENTIAL).
FT TRANSMEM 120 137 3 (POTENTIAL).

```

```

FT TRANSMEM 181 200 4 (POTENTIAL).
FT TRANSMEM 220 237 5 (POTENTIAL).
FT TRANSMEM 276 294 6 (POTENTIAL).
SQ SEQUENCE 307 AA; 33313 MW; DDC1329FEC1B4DC8 CRC64;

Query Match 50.5%; Score 778.5; DB 1; Length 307;
Best local Similarity 53.7%; Pred. No. 5,3e-62;
Matches 161; Conservative 45; Mismatches 85; Indels 9; Gaps 5;

QY 3 EQAISFAKDFLAGGIAAISKTAVPIERKLLQVQ-HASKDLADKQKGIIVDCIVRI 61
Db 7 QOETNFAINFLMGVSAIAIKTASPIERKLLQVQDEMIKGTLDKTSGLVDCPKRT 66
QY 62 PKEGVLSFWRGMLNANIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 121
Db 67 AKOEGLSFWRGMLNANIRFPTQALNFAFKDKIKLMF--GFKKEBEGYKWFAGNLASG 124
QY 122 AAGATSLCEVYPLDFAFRLADAV--GKSGTEREPKGLGDLVKTSGDIRGLYGFVS 179
Db 125 AAGATSLCEVYPLDFAFRLADAV--GKSGTEREPKGLGDLVKTSGDIRGLYGFVS 184
QY 180 SVGGIITRYRAAYFVYDTAKGML-LPDPKNTIIVYSMMIAQVTYAVGVSPPTVRRM 238
Db 185 SVGGIITRYRAAYFVYDTAKGML-LPDPKNTIIVYSMMIAQVTYAVGVSPPTVRRM 244
QY 239 MMSGKRGADIMYGTVDWCKRIFRDEGKAFKFGKANSNVLKRGMGAFVLYDELKVI 298
Db 245 MMTSGQA---VKNNGALDCKIKTIVASGVSLKGGCANILRSVAGAGVSMYDQML 301

RESULT 14
ADT_CHLRE STANDARD: PRT: 308 AA.
AC P27080;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
GN ABT.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadales; Chlamydomonas.
OX NCBI_TaxID=3055;
RN 11
RP SEQUENCE FROM N.A.
RA STRAIN=FUD4-R2;
RC STRAIN=FUD4-R2;
RX MEDLINE=93204887; PubMed=8455552;
RT Sharpe J.A., Day A.;
RT "Structure, evolution and expression of the mitochondrial ADP/ATP
translocator gene from Chlamydomonas reinhardtii.";
RL Mol. Gen. Genet. 237:134-144(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X65194; CAA46311.1; -
DR PIR: S30259; S30259.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mltch_carrier.
DR Pfam: PF00153; mltc_carri; 3.

```

DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER: 2.
 KM Mitochondrion: Inner membrane; Repeat: Transmembrane; Transport.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 74 92 2 (POTENTIAL).
 FT TRANSMEM 116 133 3 (POTENTIAL).
 FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 217 234 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 SQ SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;
 Query Match 50.0%; Score 772; DB 1; Length 308;
 Best Local Similarity 51.8%; Pred. No. 2e-61;
 Matches 157; Conservative 55; Mismatches 81; Indels 10; Gaps 5;
 QY 1 MTEQAISEKDFLAGIAAISKTAAPIERVKLLQVO-HASKQIADKQYGVDCIV 59
 DB 1 MAKEENFVADFLAGLSAAVSKTAAPIERVKLLIONODEMIKQRLASPYKGICECV 60
 QY 60 RIPEKQGVLPFRGNLANVIRYPPQALNFARFKDKYKQJELGVDKHTQFMRYFAGNLAS 119
 DB 61 RIVREKGSGLRGNLTANVIRYPPQALNFARFKDKYKQJELGVDKHTQFMRYFAGNLAS 118
 QY 120 GGAAGATSLCFYVPLDFARTRLAAD--VGKSTEREFRGLDCLVKTSDGIRGLYOG 176
 DB 119 GGAAGAVSLFYSLDYARTRLANDAKSAKGGDRQFGLVDYRKRTIASDGIAGLYRG 178
 QY 177 FEVSVOGIIITRAAFGVYDTAKG-MLPDPKNTHTVSMIAQVTVAVAGVSPFDIVR 235
 DB 179 FNISCVGIYVYGLFGYDMDSLKPVLVGLPANNFLAFLMGITIGAGLSAPIDITR 238
 QY 236 RRMWMOGSKRGADIMYGVDCMRKIFRDEGKAPFKGMSNVLRMGAPFLVYLDELK 295
 DB 238 RRMWMTS---GSAVKNSSFRQELVKNEGKSLFKGAGNITRAVAGVLAGTDLQ 295
 QY 296 KVI 298
 DB 296 VIL 298
 RESULT 15
 ADT_SCHPO STANDARD: PRT; 322 AA.
 ID ADT_SCHPO 009188;
 DT 01-NOV-1997 (Rel. 35, Last Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 GN ANCI OR SPSC530.10C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC NCBI_TaxID=4896;
 RX NCBI_TaxID=4896;
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-96257204; PubMed-8675018;
 RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae."
 RL Gene 171:113-117(1996).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quill M.A., Rabinovitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkstrein G., Aert R., Robben J., Gymnopoulos B., Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Mambutt R., Purrelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S., Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RA "The genome sequence of Schizosaccharomyces pombe."
 RT Nature 415:871-880(2002).
 CC - FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC - SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
 CC
 DR EMBL: Z49974; CAA90275.1; -
 DR EMBL: AL023634; CAI9176.1; -
 DR InterPro: IPR002067; MLC_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; Mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER: 2.
 KM Mitochondrion: Inner membrane; Repeat: Transmembrane; Transport.
 FT TRANSMEM 28 48 1 (POTENTIAL).
 FT TRANSMEM 93 111 2 (POTENTIAL).
 FT TRANSMEM 131 151 3 (POTENTIAL).
 FT TRANSMEM 197 217 4 (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT TRANSMEM 289 309 6 (POTENTIAL).
 SQ SEQUENCE 322 AA; 35020 MW; BAC3D16A40F41AFC CRC64;
 Query Match 49.8%; Score 769; DB 1; Length 322;
 Best Local Similarity 53.6%; Pred. No. 3.9e-61;
 Matches 158; Conservative 50; Mismatches 75; Indels 12; Gaps 6;
 QY 7 SFKDFLAGIAAISKTAAPIERVKLLQVOHASKQIADK--QYGVDCIVRIK 63
 DB 26 TFEFDPMGCVSAVSKTAAPIERVKLLIONO--DEMIRAGLSHRHYGIGCECFRTAA 83
 QY 64 EGVLSFWRGNLANVIRYPPQALNFARFKDKYKQJELGVDKHTQFMRYFAGLSGAA 123
 DB 84 EGVLSLWRGNLTANVIRYPPQALNFARFKDKYKQJELGVDKHTQFMRYFAGLSGAA 142
 QY 124 GATSLCFYVPLDFARTRLADV--GKSTEREFRGLDCLVKTSDGIRGLYOGFSV 181
 DB 143 GAASLFLFYSLDYARTRLANDAKSAKGGDRQFGLVDYRKRTYRSDGLRGYRGSP 202
 QY 182 OGIIITRAAFGVYDTAKG-MLPDPKNTHTVSMIAQVTVAVAGVSPFDIVRRRMM 240
 DB 203 VGIVVYRGYVGLFGYDMDSLKPVLVGLPANNFLAFLMGITIGAGLSAPIDITR 262

OY 241 QSGRKGADIMYGTVDGWRKIETDEGGKAPFKGAMSNVLRGMGAFVLYLYDELK 295
| : : : | : | : : | : | : : | : | : : | : | : : | : | : :
Db 263 TSGEA--VKYSSSFECCGROIKAKEGARSFFPKGAGANILRGVAGAGVLSIYDYO 314

Search completed: November 12, 2002, 16:46:28
Job time : 8.67525 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:45 ; Search time 25.3617 Seconds
(without alignments)
2421.054 Million cell updates/sec

Title: US-09-393-441-33
Perfect score: 1543
Sequence: 1 MFEQAIISFAKDFLAGGIAA.....LRGMGAFLVLYDELKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	1451	94.0	298	6	Q8SQH5 Bos taurus
2	1422	92.2	298	6	Q63733 Oryctolagus
3	1421	92.1	298	11	Q919M9 Xenopus lae
4	1418	91.9	298	11	Q62164 Mus musculi
5	1409	91.3	298	13	Q9PRH1 Rana rugosa
6	1406	91.1	298	13	Q9PRH2 Rana rugosa
7	1402	90.9	298	13	Q9YIC4 Rana rugosa
8	1300	84.3	299	5	Q95VX4 Elomostigmu
9	1259	81.6	317	13	Q91336 Rana sylvat
10	1254.5	81.3	299	5	Q95S30 Drosophila
11	1235.5	80.1	300	5	Q9NHWS Lucilia cup
12	1187.5	77.0	288	5	Q44093 Drosophila
13	1183.5	76.7	288	5	Q44094 Drosophila
14	1176.5	76.2	304	5	Q25129 Halocynthia
15	1137.5	73.7	307	5	Q62526 Drosophila
16	1119	72.5	315	4	Q9HOC2 Homo sapien

17	1041	67.5	313	5	Q21103 Caenorhabd
18	1039	67.3	313	5	P91410 Caenorhabd
19	1038	67.3	300	5	Q45865 Caenorhabd
20	996	64.5	309	5	Q97470 Dictyosteal
21	993.5	64.4	300	5	Q01813 Caenorhabd
22	993	64.4	300	5	Q17407 Caenorhabd
23	973.5	63.1	318	5	Q9BJ36 Toxoplasma
24	946.5	61.3	307	8	Q9XM22 Ascaris suu
25	944	61.2	301	5	Q25692 Plasmodium
26	943	61.1	301	5	Q26006 Plasmodium
27	827	53.6	170	6	Q9X569 Sus scrofa
28	778.5	50.5	305	3	Q9P8M1 Yarrowia li
29	764	49.5	326	5	P91270 Caenorhabd
30	760	49.3	307	5	Q76286 Trypanosoma
31	759	49.2	303	3	Q74260 Candida par
32	756.5	49.0	306	5	Q18683 Caenorhabd
33	753	48.8	307	5	Q26697 Trypanosoma
34	747	48.4	306	3	P78754 Schistosom
35	744	48.2	388	10	Q49875 Lupinus alb
36	743	48.2	379	10	Q49447 Arabidopsis
37	743	48.2	386	10	P93767 Lycopersico
38	734	47.6	331	10	Q41628 Trifolium tu
39	731.5	47.4	305	3	Q9P876 Pichia jadt
40	731	47.4	317	5	Q9N647 Leishmania
41	728.5	47.2	305	3	Q9P875 Pichia jadt
42	724.5	47.0	308	3	Q8TEK7 Neocallim
43	688.5	44.6	330	10	Q9FM86 Arabidopsis
44	681.5	44.2	298	5	Q21809 Caenorhabd
45	653.5	42.4	262	10	Q9AVT6 Picea abies

ALIGNMENTS

RESULT 1
ID O8SQH5 PRELIMINARY; PRT; 298 AA.
AC O8SQH5;
DT 01-JUN-2002 (TREMURel. 21, Created)
DT 01-JUN-2002 (TREMURel. 21, Last sequence update)
DT 01-JUN-2002 (TREMURel. 21, Last annotation update)
DE Adenine nucleotide translocator 2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 11
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT Identification of possible amino acids that determine functional
RT differences in its isoforms.";
RL Mitochondrion 1:371-379(2002).
DR EMBL: AB065433; BAB84673.1;
SQ SEQUENCE 298 AA; 3295 MM; CB6897BB987B79C0 CRC64;

Query Match 94.0%; Score 1451; DB 6; Length 298;
Best Local Similarity 92.2%; Pred. No. 5e-119;
Matches 273; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
QY 1 MFEQAIISFAKDFLAGGIAAISKTRAVAPIERVKLLQVHASKQIAADKQKIVDCIVR 60
DB 1 MTTDAVSFAKDFLAGGVAALSKTRAVAPIERVKLLQVHASKQITADKQKGIIDCVVR 60
QY 61 IPKDGVSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVPKHQFMFYPFAGNLASG 120
DB 61 IPKDGVSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVPKHQFMFYPFAGNLASG 120
QY 121 GAAGATSLCEFYPLDFAFTRIAADVGSSTERFRGLDCLVTKTSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCEFYPLDFAFTRIAADVGSSTERFRGLDCLVTKTSDGIRGLYOGFSVS 180

QY 181 VGGIITRAAFVGYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPEDTVRRMM 240
 DB 181 VGGIITRAAFVGYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPEDTVRRMM 240
 QY 241 QSGRKGADIMYGTGTCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLYDELKK 296
 DB 241 QSGRKGADIMYGTGTCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLYDELKK 296

RESULT 2

046373 PRELIMINARY: PRT: 298 AA.
 AC 046373;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NC NCBL_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SKELETAL MUSCLE;
 RA Yamauchi N., Kasai M.;
 RT Identification of a 30kDa calsequestrin-binding protein, which
 RT regulates calcium release from sarcoplasmic reticulum of rabbit
 RT skeletal muscle."
 RL J. Biochem. 335:541-547(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB009386; BAA23777.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 32901 MW: 32901 MW: CAEA32C88164AD78 CRC64;

Query Match 92.2%; Score 1422; DB 6; Length 298;
 Best Local Similarity 88.9%; Pred. No. 1,7e-116;
 Matches 265; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAIISFAKDFLAGGIAAISTKTAVAPIERVKLLQVOHASKQIADKQYKIVDCYR 60
 DB 1 MTEQAIISFAKDFLAGGIAAISTKTAVAPIERVKLLQVOHASKQIADKQYKIVDCYR 60
 QY 61 IPKEGVLSTFWRGNLANVIRYPTQALNFAFKKQYKQIFLGVDKTOFWRRYFAGNLASG 120
 DB 61 IPKEGVLSTFWRGNLANVIRYPTQALNFAFKKQYKQIFLGVDKTOFWRRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPAFRTLRADAVGKSGTEREFGIGDCLVYKITSDDIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTLRADAVGKSGTEREFGIGDCLVYKITSDDIRGLYQGFVS 180
 QY 181 VGGIITRAAFVGYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPEDTVRRMM 240
 DB 181 VGGIITRAAFVGYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPEDTVRRMM 240
 QY 241 QSGRKGADIMYGTGTCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLYDELKKVI 298
 DB 241 QSGRKGADIMYGTGTCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLYDELKKVI 298

RESULT 3

0919M9 PRELIMINARY: PRT: 298 AA.
 AC 0919M9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Adenine nucleotide translocase.
 GN ANTI.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 NC NCBL_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crawford M.J., Khosrowshahian F., Yarmuza S.L., Liversage R.A.;
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
 RT dynamic Patterns of Expression During Development."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF231347; AAF63471.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 32940 MW: 91874013751877E CRC64;

Query Match 92.1%; Score 1421; DB 13; Length 298;
 Best Local Similarity 90.3%; Pred. No. 2,1e-116;
 Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAIISFAKDFLAGGIAAISTKTAVAPIERVKLLQVOHASKQIADKQYKIVDCYR 60
 DB 1 MTEQAIISFAKDFLAGGIAAISTKTAVAPIERVKLLQVOHASKQIADKQYKIVDCYR 60
 QY 61 IPKEGVLSTFWRGNLANVIRYPTQALNFAFKKQYKQIFLGVDKTOFWRRYFAGNLASG 120
 DB 61 IPKEGVLSTFWRGNLANVIRYPTQALNFAFKKQYKQIFLGVDKTOFWRRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPAFRTLRADAVGKSGTEREFGIGDCLVYKITSDDIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTLRADAVGKSGTEREFGIGDCLVYKITSDDIRGLYQGFVS 180
 QY 181 VGGIITRAAFVGYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPEDTVRRMM 240
 DB 181 VGGIITRAAFVGYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPEDTVRRMM 240
 QY 241 QSGRKGADIMYGTGTCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLYDELKKVI 298
 DB 241 QSGRKGADIMYGTGTCWKRIFRDEGKAFKFGAMSNVLRGMGAFVLYDELKKVI 298

RESULT 4

062164 PRELIMINARY: PRT: 298 AA.
 AC 062164;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Adenine nucleotide carrier (Adenine nucleotide translocase 1) (Similar
 DE to solute carrier family 25 (Mitochondrial carrier, adenine nucleotide
 DE translocator), member 4) (Hypothetical 32.9 kDa protein).
 GN SLC25A4 OR MNC1 OR ANTI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 NC NCBL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=MUSCLE;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.:
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 RT translocase 1 and 2 genes."
 RN Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.:
 RL Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EYE.
 RA Strausberg R.:
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC EMBL: X74510; CA52616.1; -.
 DR EMBL: AF240002; AAF64470.1; -.
 DR EMBL: BC026925; AAH26925.1; -.
 DR MGD: MGI:1353495; SLC25a4.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carr.3
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Hypothetical protein; Inner membrane; Repeat; Transmembrane;
 KW Transport; Mitochondrion.
 SQ SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match 91.9%; Score 1418; DB 11; Length 298;
 Best Local Similarity 88.9%; Pred. No. 3.9e-116;
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

OY 1 MTEQATSFPAKDFLAGIAAISTAVAPIERVKLLQVOHASKOIAADKQYKIVDCIYR 60
 DB 1 MDDQALSFKDFLAGIAAISTAVAPIERVKLLQVOHASKOIAAEKQYKIIDCVYR 60
 OY 61 IREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKTQFWRYPAGMLASG 120
 DB 61 IREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKTQFWRYPAGMLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGKSGEREFGGLGCLVITKSDGKGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKSGEREFGGLGCLVITKSDGKGLYQGFVS 180
 OY 181 VGGIIRYRAAFGVYDTAKGMLPDPKNTHTIVSMIAQTAVAGVSYPFDTVRRRMM 240
 DB 181 VGGIIRYRAAFGVYDTAKGMLPDPKNTHTIVSMIAQTAVAGVSYPFDTVRRRMM 240
 OY 241 OSGRKADIMYGTVDCKRKIFRDEGKAFKFGAMSNTLRGMGAFVLVLYDELKRYI 298
 DB 241 OSGRKADIMYGTVDCKRKIFRDEGKAFKFGAMSNTLRGMGAFVLVLYDEIKRYV 298
 RESULT 5
 O9PRH1 PRELIMINARY; PRT; 298 AA.
 AC O9PRH1:
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9083429; PubMed=9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.:
 DR "The origin and differentiation of the heteromorphic sex chromosomes
 RT

RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC EMBL: AB008463; BAA36513.1; -.
 DR EMBL: AB008456; BAA36506.1; -.
 DR EMBL: AB008461; BAA36511.1; -.
 DR EMBL: AB008462; BAA36512.1; -.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mito_carr.3
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33054 MW; B0E23AD565F548D36 CRC64;

Query Match 91.3%; Score 1409; DB 13; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.4e-115;
 Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

OY 1 MTEQATSFPAKDFLAGIAAISTAVAPIERVKLLQVOHASKOIAADKQYKIVDCIYR 60
 DB 1 MDDAATSFPAKDFLAGIAAISTAVAPIERVKLLQVOHASKOITRADKQYKIMCCVYR 60
 OY 61 IREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKTQFWRYPAGMLASG 120
 DB 61 IREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLDVNDKRTQFWRYPAGMLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGKSGEREFGGLGCLVITKSDGKGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGADREFKGLGCLVITKSDGKGLYQGFVS 180
 OY 181 VGGIIRYRAAFGVYDTAKGMLPDPKNTHTIVSMIAQTAVAGVSYPFDTVRRRMM 240
 DB 181 VGGIIRYRAAFGVYDTAKGMLPDPKNTHTIFISMTIAQTAVAGVSYPFDTVRRRMM 240
 OY 241 OSGRKADIMYGTVDCKRKIFRDEGKAFKFGAMSNTLRGMGAFVLVLYDELKRYI 298
 DB 241 OSGRKAEIMYSTICWKRIARDEGSRAFKFGAMSNTLRGMGAFVLVLYDELKRYI 298
 RESULT 6
 O9PRH2 PRELIMINARY; PRT; 298 AA.
 AC O9PRH2:
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9083429; PubMed=9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.:
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC EMBL: AB008460; BAA36510.1; -.
 DR EMBL: AB008458; BAA36508.1; -.
 DR EMBL: AB008459; BAA36509.1; -.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.

DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane: Mitochondrion; Transmembrane: Transport.
 SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 91.1%; Score 1406; DB 13; Length 298;
 Best Local Similarity 88.3%; Pred. No. 4,4e-115;
 Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEGAISFADFLAGIAAIAISKTAAPIERVKLLLOVHAASKOITADKQKIGIMDCVVR 60
 DB 1 MTEGAISFADFLAGIAAIAISKTAAPIERVKLLLOVHAASKOITADKQKIGIMDCVVR 60
 QY 61 IPKEQGLSEFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 DB 61 IPKEQGLSEFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCEVYPLDFARTRLADVGKSGTEREPRGIGDCLVTKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCEVYPLDFARTRLADVGKAGADREFKGLGDCIAKIFRSDGILKGLYQGFVS 180
 QY 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMTAQTYTAVAGVSYPPDYRRRMM 240
 DB 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMTAQTYTAVAGVSYPPDYRRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWKRIFRDEGKAFKFGAMS NVLKGMGAFVLYLYDELKQYI 298
 DB 241 QSGRKGAEIMYSGTIDCWKKIARDEGSRAPFKGMS NVLKGMGAFVLYLYDELKQYI 298

RESULT 7
 QYIC4 PRELIMINARY; PRT; 298 AA.
 ID 09YIC4
 AC 09YIC4:
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Frogs).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99083429; PubMed=9866197;
 RA Mura T., Ohnishi H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromeric sex chromosomes of z, w, x, and y in the frog Rana rugosa. Inferred from the sequences of a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619 (1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY)
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008457; BA36507.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane: Mitochondrion; Transmembrane: Transport.
 SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 90.9%; Score 1402; DB 13; Length 298;
 Best Local Similarity 87.9%; Pred. No. 9,8e-115;
 Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MTEGAISFADFLAGIAAIAISKTAAPIERVKLLLOVHAASKOITADKQKIGIMDCVVR 60
 DB 1 MTEGAISFADFLAGIAAIAISKTAAPIERVKLLLOVHAASKOITADKQKIGIMDCVVR 60

DB 1 MTEGAISFADFLAGIAAIAISKTAAPIERVKLLLOVHAASKOITADKQKIGIMDCVVR 60
 QY 61 IPKEQGLSEFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 DB 61 IPKEQGLSEFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCEVYPLDFARTRLADVGKSGTEREPRGIGDCLVTKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCEVYPLDFARTRLADVGKAGADREFKGLGDCIAKIFRSDGILKGLYQGFVS 180
 QY 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMTAQTYTAVAGVSYPPDYRRRMM 240
 DB 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMTAQTYTAVAGVSYPPDYRRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWKRIFRDEGKAFKFGAMS NVLKGMGAFVLYLYDELKQYI 298
 DB 241 QSGRKGAEIMYSGTIDCWKKIARDEGSRAPFKGMS NVLKGMGAFVLYLYDELKQYI 298

RESULT 8
 Q95VX4 PRELIMINARY; PRT; 299 AA.
 ID 095VX4
 AC 095VX4:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP-ATP translocator.
 OS Echinostigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda; Chilopoda; Pleurostigmophora; Scolopendromorpha; Scolopendridae; Echinostigmus.
 OX NCBI_TaxID=62613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burnell J.N.;
 RT "Nucleotide sequence of an ADP-ATP translocator of Echinostigmus rubripes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF401758; AL02100.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN 2.
 SQ SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E CRC64;

Query Match 84.3%; Score 1300; DB 5; Length 299;
 Best Local Similarity 81.5%; Pred. No. 8,5e-106;
 Matches 243; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

QY 1 MTEGAISFADFLAGIAAIAISKTAAPIERVKLLLOVHAASKOITADKQKIGIMDCVVR 60
 DB 1 MTEGAISFADFLAGIAAIAISKTAAPIERVKLLLOVHAASKOITADKQKIGIMDCVVR 60
 QY 61 IPKEQGLSEFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 DB 61 IPKEQGLSEFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCEVYPLDFARTRLADVGKSGTEREPRGIGDCLVTKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCEVYPLDFARTRLADVGKAGADREFKGLGDCIAKIFRSDGILKGLYQGFVS 180
 QY 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMTAQTYTAVAGVSYPPDYRRRMM 240
 DB 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMTAQTYTAVAGVSYPPDYRRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWKRIFRDEGKAFKFGAMS NVLKGMGAFVLYLYDELKQYI 298
 DB 241 QSGRKGADIMYTGTVDCWKRIFRDEGKAFKFGAMS NVLKGMGAFVLYLYDELKQYI 298

RESULT 9
 Q91336 PRELIMINARY; PRT; 317 AA.
 ID 091336
 AC 091336:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana sylvatica (wood frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 NX NCBI_TaxID=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=97398141; PubMed=9256066;
 RA Cal O., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 in wood frogs under freezing stress.";
 RT Biochim. Biophys. Acta 1353:69-78(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX Cal O., Storey K.B.;
 RT Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: U44832; AAA97882.2; -;
 DR InterPro: IPR001993; Mitoch_carrler.
 DR InterPro: IPR002067; Mito_carrler.
 DR Pfam: PF00153; Mito_carr; 3.
 DR PRINTS: PRO0926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;

Query Match 81.6%; Score 1259; DB 13; Length 317;
 Best Local Similarity 86.8%; Pred. No. 3.6e-102;
 Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

OY 1 MTEQISFAKDFLAGGIAAISKTAVERKLLQVOHASKOIAAKQYKIVDCIYR 60
 DB 1 MTDAAANSRAKDFLAGGAAIAISKTAVERKLLQVOHASKOITADQYKIGIMDCVVR 60
 OY 61 IPKEGVLSPFWRGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYPAGNLASG 120
 DB 61 IPKEGVLSPFWRGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYPAGNLASG 120
 OY 121 GAAGATSLCFYVPLDFAKRLADVGKSGTEREPGLDCLVTKISDGIKGLYGFYSV 180
 DB 121 GAAGATSLCFYVPLDFAKRLADVGKSGTEREPGLDCLVTKISDGIKGLYGFYSV 180
 OY 181 VOGIITVRAAYGVYDTAKGMLPDPKNTIIVSMMIAQTVTVAGVSVPPDTRRRMM 240
 DB 181 VOGIITVRAAYGVYDTAKGMLPDPKNTIIVSMMIAQTVTVAGVSVPPDTRRRMM 240
 OY 241 QSGRKADIMYTGVDCKMKIFRDEGKAFFK 272
 DB 241 QSGRKAEIMYSGTIDCKMKIARDEGGAFFR 272
 RESULT 10
 Q93S30 PRELIMINARY; PRT; 299 AA.
 AC Q93S30;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE GM12886P (LP02726P).
 GN SE8B OR CG16944.
 OS Euxophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacled J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacled J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceiniker S.;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY060978; AAL28526.1; -;
 DR EMBL: AY070894; AAL48516.1; -;
 DR FlyBase: FBgn0003360; se8B.
 DR InterPro: IPR001993; Mitoch_carrler.
 DR Pfam: PF00153; mito_carr; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_3.
 SQ SEQUENCE 299 AA; 32909 MW; D51FE3E2A70BD59E8 CRC64;

Query Match 81.3%; Score 1254.5; DB 5; Length 299;
 Best Local Similarity 80.6%; Pred. No. 8.2e-102;
 Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;

OY 5 AISPFAKDFLAGGIAAISKTAVERKLLQVOHASKOIAADQYKIVDCIYR 64
 DB 7 AVGFVKDFAGGISAASVSTAVAPIERKLLQVOHISQISPDQYKQWVCFRIPIRE 66
 OY 65 QGVLSFWRGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYPAGNLASGAAG 124
 DB 67 QGVLSFWRGNLANVIRYPTQALNFAFKDKYQIFLGVDKHTQFWRYPAGNLASGAAG 126
 OY 125 ATSLCFYVPLDFAKRLADVGKSGTEREPGLDCLVTKISDGIKGLYGFYSV 184
 DB 127 ATSLCFYVPLDFAKRLADVGKSGTEREPGLDCLVTKISDGIKGLYGFYSV 185
 OY 185 IIVRAAYGVYDTAKGMLPDPKNTIIVSMMIAQTVTVAGVSVPPDTRRRMMQSGR 244
 DB 186 IIVRAAYGVYDTAKGMLPDPKNTIIVSMMIAQTVTVAGVSVPPDTRRRMMQSGR 245
 OY 245 KQADIMYTGVDCKMKIFRDEGKAFFKGAWSNVLKMGGAFLVLYDELKVI 298
 DB 246 KATEVIYKNTLHCWATIAKQEGTGAFKGAFFSNILKGTGAFVLVLYDEIKKVL 299
 RESULT 11
 Q9NHM5 PRELIMINARY; PRT; 300 AA.
 AC Q9NHM5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Lucilia cuprina (Australian sheep blowfly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Oestroidea; Calliphoridae; Lucilia.
 NX NCBI_TaxID=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS MAL SEEKING;
 RA Chen Z., Fair J.A., Batterham P.;
 RT "A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF218587; AAF32322.1; -;
 DR InterPro: IPR001993; Mitoch_carrler.

DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 300 AA: 33036 MW: 5459DFOBA0E2E742 CRC64;

Query Match 80.1%; Score 1235.5; DB 5; Length 300;
 Best Local Similarity 79.5%; Pred. No. 3.8e-100;
 Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;

QY 6 ISPAKDFLAGGIAAISKTAIVAPIERVKLLQVOHASKQIADKOYGIYDCIIRPEKQ 65
 DB 9 LGFVKDPAAGGISAASVKTAVAPIERVKLLQVOHISKQISPKQYKGMIDCFVRIPEKQ 68
 QY 66 GVSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHTQFMRYFAGNLASGAAGA 125
 DB 69 GFASVWRGNMANVIRYPTQALNFAFKDKYKQVFLGVDKNTQFMRYFAGNLASGAAGA 128
 QY 126 TSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVKTIKSDGIRGLYOGFSVVOGII 185
 DB 129 TSLCFYVPLDFARTRLAADVGKSG-QREFTGNGNCLAKIFKSDGLVGLYRGFVVOGII 187
 QY 186 IYRAAFEGYVDPAKGMIDPKKNTHTIVSMIAQVTAVAGVSYFPDVTVRMMQSGRK 245
 DB 188 IYRAAFEGYVDPAKGMIDPKKNTHTIVSMIAQVTVAGIVSYFPDVTVRMMQSGRK 247
 QY 246 GADIMYTGVDCKRKIFRDEGKAFKFGKAMSNVLKGMGAFVLVYDELKKVI 298
 DB 248 ATEIIYKNTIHCWATIAKQEGTGAFKFGKAMSNVLKGTGAFVLVYDELKKFL 300

RESULT 12
 ID 044093 PRELIMINARY; PRT; 288 AA.
 AC 044093;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila pseudobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetica 0:0-0(1997).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF025798; AAB87883.1; -.
 DR FlyBase: FBgn0023292; DpseLsesB.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 SQ SEQUENCE 288 AA: 31725 MW: 052B0CC0050436B0 CRC64;

Query Match 77.0%; Score 1187.5; DB 5; Length 288;
 Best Local Similarity 80.7%; Pred. No. 5.8e-96;
 Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3;

QY 5 AIFSAKDFLAGGIAAISKTAIVAPIERVKLLQVOHASKQIADKOYGIYDCIIRPEK 64
 DB 7 AIFGVDFAGGISAASVKTAVAPIERVKLLQVOHISKQISPKQYKGMIDCFVRIPEK 66
 QY 65 QGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHTQFMRYFAGNLASGAAG 124

DB 67 QGVSSFWKGNLANVIRYPTQALNFAFKDKYKQVFLGVDKNTQFMRYFAGNLASGAAG 126
 QY 125 ATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVKTIKSDGIRGLYOGFSVVOGI 184
 DB 127 ATSLCFYVPLDFARTRLAADVGKSG-QREFTGNGNCLTKIFKSDGLVGLYRGFVVOGI 185
 QY 185 IYRAAFEGYVDPAKGMIDPKKNTHTIVSMIAQVTAVAGVSYFPDVTVRMMQSGRK 244
 DB 186 IYRAAFEGYVDPAKGMIDPKKNTHTIVSMIAQVTVAGIVSYFPDVTVRMMQSGRK 244
 QY 245 KGADIMYTGVDCKRKIFRDEGKAFKFGKAMSNVLKGMGAFVLV 289
 DB 245 KATEIIYKNTIHCWATIAKQEGTGAFKFGKAMSNVLKGTGAFVLV 288

RESULT 13
 ID 044094 PRELIMINARY; PRT; 288 AA.
 AC 044094;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila subobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetica 0:0-0(1997).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF025799; AAB87884.1; -.
 DR FlyBase: FBgn0023237; DsubLsesB.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 SQ SEQUENCE 288 AA: 31775 MW: 06A1DIE477E81B26 CRC64;

Query Match 76.7%; Score 1183.5; DB 5; Length 288;
 Best Local Similarity 80.4%; Pred. No. 1.3e-95;
 Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

QY 5 AIFSAKDFLAGGIAAISKTAIVAPIERVKLLQVOHASKQIADKOYGIYDCIIRPEK 64
 DB 7 AMGVKDFEAGGISAASVKTAVAPIERVKLLQVOHISKQISPKQYKGMIDCFVRIPEK 66
 QY 65 QGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHTQFMRYFAGNLASGAAG 124
 DB 67 QGVSSFWKGNLANVIRYPTQALNFAFKDKYKQVFLGVDKNTQFMRYFAGNLASGAAG 126
 QY 125 ATSLCFYVPLDFARTRLAADVGKSGTEREFGDCLVKTIKSDGIRGLYOGFSVVOGI 184
 DB 127 ATSLCFYVPLDFARTRLAADVGKSG-QREFTGNGNCLTKIFKSDGLVGLYRGFVVOGI 185
 QY 185 IYRAAFEGYVDPAKGMIDPKKNTHTIVSMIAQVTAVAGVSYFPDVTVRMMQSGRK 244
 DB 186 IYRAAFEGYVDPAKGMIDPKKNTHTIVSMIAQVTVAGIVSYFPDVTVRMMQSGRK 244
 QY 245 KGADIMYTGVDCKRKIFRDEGKAFKFGKAMSNVLKGMGAFVLV 289
 DB 245 KATEIIYKNTIHCWATIAKQEGTGAFKFGKAMSNVLKGTGAFVLV 288

00 Ephydroidea: Drosophilidae: Drosophila.
01 NCBI_TaxID=7227;
02 [1]
03 RP SEQUENCE FROM N.A.
04 RC STRAIN=BERKELEY;
05 RX MEDLINE=20196006; PubMed=10731132;
06 RA Adams M.D., Gelhiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
07 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
08 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
09 Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
10 Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
11 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
12 Abail J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
13 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
14 Beeson K.Y., Bessio P.V., Berman B.P., Bhandari D., Bolshakov S.,
15 Borkovs D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
16 Burkula K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
17 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
18 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
19 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
20 Durbin K.J., Evangelista C.C., Ferriz C., Ferreira S., Fleischmann W.,
21 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
22 Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
23 Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
24 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
25 Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
26 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
27 Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
28 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
29 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
30 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
31 Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclob J.M.,
32 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
33 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
34 Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
35 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
36 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
37 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissensbach J.,
38 Williams M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
39 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
40 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
41 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
42 RT "The genome sequence of Drosophila melanogaster."
43 RT Science 287:2185-2195(2000).
44 [2]
45 RP SEQUENCE FROM N.A.
46 RC STRAIN=OREGON-R;
47 RL Zhang Y.Q., Davis A.W., Roote J., Ashburner M.;
48 Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
49 DR EMBL: AE003484; AAF47956.1; -
50 DR EMBL: Y10618; CAAT71629.1; -
51 DR FLYBase: FBgn0025111; Ant2.
52 DR InterPro: IPR001993; Mitoch_carrier.
53 DR InterPro: IPR002067; Mit_carrier.
54 DR Pfam: PF00153; mito_carr; 3.
55 DR PRINTS: PR00926; MITOCARRIER.
56 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN.2.
57 SEQUENCE 307 AA: 33744 MW: 3063BDPFB2061COC CMC64;
01
02
03
04
05
06
07
08
09
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544

